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CC	EMBL; Z15028; CAA78747.1; --	
DR	EMBL; X64770; CAA46017.1; --	
DR	PIR; S23543; S23543.	
DR	Gramene; P30298; --	
DR	InterPro; IPR001296; Glyco_trans 1.	
DR	InterPro; IPR000368; Sucrose synth.	
DR	Pfam; PF00534; Glycos_transf_1; 1.	
DR	Pfam; PF00862; Sucrose_synth; 1.	
KW	transferase; Glycosyltransferase; Multigene family.	
FT	CONFLICT 191 191	
SO	SEQUENCE 808 AA; 921113 MW; 3BF529E98686AB71 CRC64;	
	P -> L (IN REF. 2).	

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Qy      777 RYLEMYIILKREELAKTVPLAID 799
Db      780 RYTEMFYALKYRSLASAVPLAVD 802

RESULT 10
SUSL_TUJGE STANDARD; PRT; 805 AA.
AC Q41608;
Dt DT 15-DEC-1998 (Rel. 37, Created)
Dt DT 15-DEC-1998 (Rel. 37, Last sequence update)
Dt DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DE Sucrose synthase 1 (EC 2.4.1.13) (Sucrose=UDP glucosyltransferase 1).
OS Tulipa gesneriana (Tulip).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
OX Tulipa.
OX NCBI_TaxID=13306;
RN [1]
SEQUENCE FROM N.A.
RP RC STRAIN=cv. Apeidoorn;
RA RA Balk P.A., de Boer A.D.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -i FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC CC -i CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC CC -i SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
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CC EMBL; X96938; CAA65639.1; -.
DR DR InterPro; IPR001296; Glyco_trans_1.
DR DR InterPro; IPR003368; Sucrose synth.
DR DR Pfam; PF00534; Glycos transf 1; 1.
DR DR Pfam; PF00862; Sucrose synth; 1.
KW KW Transferase; Glycosyltransferase; Multigene family.
SQ SEQUENCE 805 AA; 92554 MW; B749D8953C9338F0 CRC64;

Query Match          70.7%; Score 2982; DB 1; Length 805;
Best local Similarity 69.9%; Pred.No. 5.6e-191;
Matches 558; Conservative 112; Mismatches 124; Indels 4; Gaps 3;

Qy      3 HASGDRVEDTLNHRNELVALLSKYVNGKGILLDPHILDALDVEQSGGR-ALAEGPFL 61
Db      10 HSIKERIGDSLHHNPENLLAFGRFIQGGKGLRHOULTYEYSVIPEDAREKLKDGVE 69

Qy      62 DVLRSAQEALVPFPFAIAVRPGWWEYVRYNNVNHLSVEQLTYSELYRKFKEELVDGOHN 121
Db      70 DTLEASQEALVIPFWVALAIRPGWWEYVRYNNVELAVEE--CSEYLKFKELDVDRSSQ 127

Qy      122 DPYYLELDFFPNVSVPRPNRSSISGNVGQVLNRHLSSIMPRNRDCLEPLLDFRGRRHK 181
Db      128 SNFVLEMDFFPNANVRPRSLSISGNVGQVLNRHLSSKLPFHDKESLYPLNFLREHNYK 187

Qy      182 GHVWMINDRTQSILQGLOSLVTKAEEHLSKLPAADTPYSQA VKFOEWGLEKMGWDTAGHVL 241
Db      188 GTTMLNDRLQSLSALQTALRKADRYLLISKUTPYSEFNHS FQVLGLEKMGWDTSRVS 247

Qy      242 EMIEHLLDIIOAPPSPSTLEKFLGRIPMI FNVVVSPHYGFAQNLGLPDGTGGQIVYILD 301
Db      248 ENIHLLDLLEAPDPSTLEKFLGTIPMWNVVILSPHYGAQANLVGYPDGTGGQVYILD 307

Qy      302 QVRALENEMVLRKKQGLDVSPKXLI VTRLPIDPAKAGTSCNORLERISTQHTYILIRVPPR 361
Db      108 OVRALETMLAKIKOOGGLDTPIRLI VTRLLPDVAVGTTCGORLBRVLGTETHIIRVFR 367

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RESULT 12	
SUS3_ORYSA	STANDARD; PRT; 816 AA.
AC Q43009;	
DT 15-DEC-1998 (Rel. 37, Created)	
DT 15-DEC-1998 (Rel. 37, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Sucrose synthase 3 [EC 2.4.1.13] (Sucrose-UDP glucosyltransferase 3).	
GN SS3.	
OS Oryza sativa (Rice).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC Ehrhartoideae; Oryzaceae; Oryza.	
OX NCBI_TaxID=4530;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Tainong 67; T-SUSE=Leaf, and Root;	
RX MEDLINE=97076616; PubMed=9063969;	
RA Huang J.W., Chen J.C., Yu M.P., Shyur L.F., Wang A.Y., Sung H.Y.,	
RA Lee P.D., Su J.C.;	
RT "Complete structures of three rice sucrose synthase isogenes and	
RT differential regulation of their expressions.";	
RL Biosci. Biotechnol. Biochem. 60:233-239 (1996).	
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and	
CC fructose for various metabolic pathways.	
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.	
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant	
CC sucrose synthase subfamily.	
CC	
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CC	
CC EMBL; L03366; AAC41682.1; -.	
DR Gramene; O43009; -.	
DR InterPro; IPR001296; Glyco trans 1.	
DR InterPro; IPR000368; Sucrose synth.	
DR Pfam; PF00534; Glycos. trans 1; 1.	
DR Pfam; PF00862; Sucrose synth; 1.	
KW Transferrase; Glycosyltransferase; Multi-gene family.	
SEQUENCE 816 AA; 93209 MW; 485817C106A77D2A CRC64;	
Query Match 69.98; Score 2948; DB 1; Length 816;	
Best Local Similarity 68.24; Pred. No. 1.1e-188;	
Matches 544; Conservative 119; Mismatches 133; Indels 2; Gaps 2;	
QY 3 HADGRVETLHARNELVALLSKYVNGKGILOPHHILDALDEVQSGGR-ALAEQFEL 61	
DB 14 HSWRERIGDSLSAHTNELVAFSLVNGKGMQLPHQIIAEYNAIIPGEREKLDKSALE 73	
QY 62 DVLRSAGEAIVLPFPFAIAVRPGVWYKRVNWHLSVQLTVSEYLRFKBELVDGQHN 121	
DB 74 DVLRSAGEAIVLPFPFAIAVRPGVWYKRVNWHLSVQLTVSEYLRFKBELVDGQHN 133	
QY 122 DPVYLEDFEPFNVSVPNRPSSISNGVQFLNHLSSIMFERNDCLEPLDLRGRHK 181	
DB 134 KNFVLELDFEPFNVSVPNRPSSISNGVQFLNHLSSIMFERNDCLEPLDLRGRHK 193	
QY 182 GHWMLNDRIOSGLRSLVTKAEHLSKLPADTPYSQFAYKQFQEWGLEKGGDTAGHVL 241	
DB 194 GHWMLNDRIOSGLRSLVTKAEHLSKLPADTPYSQFAYKQFQEWGLEKGGDTAGHVL 253	
QY 242 EMHLLDIIQAPDSTLEKELGRIPMIFNVVSPHGYFQGANVLGIPDTGGQIVILD 301	
DB 254 ETIHLLDIIQAPDSTLEKELGRIPMIFNVVSPHGYFQGANVLGIPDTGGQIVILD 313	
QY 302 QVRALENEXYLRKQGLVDSPKILIVTRLPDAKGISCNQRLERISTQHTYILRVFPR 361	

Db	314	QVRALENEXYLRKQGLVDSPKILIVTRLPDAKGISCNQRLERISTQHTYILRVFPR	373
QY	362	MENGILKKWISRPDVPWPLYLETFAEDAAGIAELAQTPDFFIIGNYSDGNLVALSYKMG	421
Db	374	TENGTVRKWISRPDVPWPLYLETFAEDAAGIAELAQTPDFFIIGNYSDGNLVALSYKMG	433
QY	422	ITQCNIAHALEKTKYPSDSDIFKWNDEKHFSCQFTADIIAMNADFIITSTQETAGSK	481
Db	434	VTHCTTAHALEKTKYPSDSDIFKWNDEKHFSCQFTADIIAMNADFIITSTQETAGSK	493
QY	482	NTVGQVESHATAFLPGLYRVVHGIDVDFPKFNVSPGADMSIYFPHTEKAKRLTSLFSG	541
Db	494	ETVGQVESHATAFLPGLYRVVHGIDVDFPKFNVSPGADMSIYFPHTEKAKRLTSLFSG	553
QY	542	ENLIYDPEQNDHGHLDKDRSPILFSMARLDKVNKTIGLVEAFKAKLRELNVLVVA	601
Db	554	EELLPSDVENTEKKFVLKDKKKPIIFSMARLDKVNKTIGLVEAFKAKLRELNVLVVA	613
QY	602	GYNVNVKSKOREIAEIKWHELIKTNLFQGFQFVWISACTNARNGELVRYIADTHGAFV	661
Db	614	G-DHGKESKOREIAEIKWHELIKTNLFQGFQFVWISACTNARNGELVRYIADTHGAFV	672
QY	662	QPALYEAFLGTVVEMTCGLPTFATLHGPGPAEIIIEHGVSGFHIDPYHPEQAVNLMADFPD	721
Db	673	QPALYEAFLGTVVEMTCGLPTFATLHGPGPAEIIIEHGVSGFHIDPYHPEQAVNLMADFPD	732
QY	722	RKQDPDHWNVISGAGLQRIEYKTKWIKYSERLMTLAGYGFVKYKSLERLETRRYLEM	781
Db	733	KCEDPNHWIKISQGGLORIEYKTKWIKYSERLMTLAGYGFVKYKSLERLETRRYLEM	792
QY	782	FYILKPRELAKTVPLAID 799	
Db	793	LYALKYRKQATVPLAIE 810	

RESULT 13

SUS1_SOLTU	STANDARD; PRT; 805 AA.
ID -SUS1_SOLTU	
AC P10691;	
DT 01-JUL-1989 (Rel. 11, Created)	
DT 01-JUL-1989 (Rel. 11, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase)	
DE (SS16).	
OS Solanum tuberosum (Potato).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	
OC Lamiales; Solanales; Solanaceae; Solanum.	
OX NCBI_TaxID=4113;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Sirtama;	
RX MEDLINE=86152501; PubMed=2964386;	
RA Salanoubat M., Belliard G.;	
RT "Molecular cloning and sequencing of sucrose synthase cDNA from	
RT potato (Solanum tuberosum L.): preliminary characterization of	
RT sucrose synthase mRNA distribution.";	
RL Gene 60:47-56 (1987).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC STRAIN=cv. FL1607; TISSUE=Leaf;	
RX MEDLINE=96172787; PubMed=8589622;	
RA Fu H., Park W.D.;	
RT "Sink- and vascular-associated sucrose synthase functions are encoded	
RT by different gene classes in potato.";	
RL plant Cell 7:1369-1385 (1995).	
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and	
CC fructose for various metabolic pathways.	
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.	
CC -!- TISSUE SPECIFICITY: Expression is at least 10 fold higher in	
CC tubers compared to photosynthetically active tissues.	
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant	

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CC sucrose synthase subfamily.
CC -----
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CC -----
CC EMBL; M18745; AAA33841.1; -
CC EMBL; U24C87; AAA97571.1; -
CC PIR; A29615; YUPOS.
CC InterPro; I2R001296; Glyco_trans_1.
CC InterPro; I2R000368; Sucrose synth.
CC Pfam; PF00534; Glycos_transf_1; 1.
CC Pfam; PF00862; Sucrose synth; 1.
CC Transferrase; Glycosyltransferase; Multigene family.
KW CONFLICT 221 221 KD -> D (IN REF. 2).
FT CONFLICT 731 732 KD -> RE (IN REF. 2).
FT CONFLICT 741 741 M -> T (IN REF. 2).
FT CONFLICT 748 748 E -> Q (IN REF. 2).
FT CONFLICT 759 759 S -> R (IN REF. 2).
SQ SEQUENCE 805 AA; 92416 MW; C453363A7CD32869 CRC64;

Query Match 69.8%; Score 2944.5; DB 1; Length 805;
Best Local Similarity 69.0%; Pred.No.1.8e-188;
Matches 549; Conservative 115; Mismatches 132; Indels 1; Gaps 1;

QY 3 HASGERVEDTTHAHNELVALLSKYVNGKGILOPHHILDALDVEQSGGRALAEQGFLD 62
DB 10 HSLERVDATLAHRNEILLFLSRSHGKILKPHELLAFAFDALRQDDKKNLNEHAFEE 69

QY 63 VLRSQAQAIPLPPFVAIAVRPRPGWVEYRVNHNLSVEQLTVSEYLRKFKEELVDGQND 122
DB 70 LLKSTQEAIVLPPWVALAIRLRPGWVEYRVNHNLSVEQLTVSEYLRKFKEELVDGASNG 129

QY 123 PYVLELDEPFPNVSPRNRSSISGNGVQFNLNRHLSIMFRNRDCLPLDLFGRHRHG 182
DB 130 NFVLELDEPFPSTAPFKPTLTGKISGNGVEFNLNRHLSAKMFHDKESMAPLLEFRAHYNG 189

QY 183 HVMLNDRISQIGRLQSVLTAKAEHLSKLPADTPYSQFAYKPFQEWGLEKMGWDTAGHVLE 242

Query Match 69.8%; Score 2944.5; DB 1; Length 805;
Best Local Similarity 69.0%; Pred.No.1.8e-188;
Matches 550; Conservative 114; Mismatches 132; Indels 1; Gaps 1;

QY 3 HASGERVEDTTHAHNELVALLSKYVNGKGILOPHHILDALDVEQSGGRALAEQGFLD 62
DB 10 HSLERVDATLAHRNEILLFLSRSHGKILKPHELLAFAFDALRQDDKKNLNEHAFEE 69

QY 63 VLRSQAQAIPLPPFVAIAVRPRPGWVEYRVNHNLSVEQLTVSEYLRKFKEELVDGQND 122
DB 70 LLKSTQEAIVLPPWVALAIRLRPGWVEYRVNHNLSVEQLTVSEYLRKFKEELVDGASNG 129

QY 123 PYVLELDEPFPNVSPRNRSSISGNGVQFNLNRHLSIMFRNRDCLPLDLFGRHRHG 182
DB 130 NFVLELDEPFPSTAPFKPTLTGKISGNGVEFNLNRHLSAKMFHDKESMAPLLEFRAHYNG 189

QY 183 HVMLNDRISQIGRLQSVLTAKAEHLSKLPADTPYSQFAYKPFQEWGLEKMGWDTAGHVLE 242

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Db 190 KTWMLNDRIHNSNTLQNLVLRKABEYLIMLPETPTFFEEHKEFQBLEKGWGDTAERVLE 249
 Qy 243 MIHLLLDIIQAPDSTLEKFLGRIPMLFNVVVSPHSGYFGQANVLGPDGTGGQIVYILDQ 302
 Db 250 MWCMLLDLEAPDSTLEKFLGRIPMLFNVVVSPHSGYFGQANVLGPDGTGGQIVYILDQ 309
 Qy 303 VRALENEMWRLKKGGLDVSFKILIVRLIPDAGTSCNORLERISGTOHTYILRVFERN 362
 Db 310 VPAEREMLRKRIKQGGJIPRIILIVRLPDAGTTCGQRLKLYGTEHSHILRVFPFT 369
 Qy 363 ENGLKWKWISRFDPWVPLETFAEDAAGEIAAELQCTPDIIGNYSDGNLVAISLKYKGI 422
 Db 370 EKGIVRWISRFEPWVPLETFAEDAAGEIAAELQCTPDIIGNYSDGNLVAISLKYKGI 429
 Qy 423 TQCMIAHALEKTKYPDSDI FWNKDEKXHFSCQPTADIIAMNADFIITSTYQBIAGSKN 482
 Db 430 TQCTIAHALEKTKYPDSDI FWNKDEKXHFSSQPTADIIAMNADFIITSTYQBIAGSKN 489
 Qy 483 TVGQYSEHTAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKRLTSLHGSIE 542
 Db 490 TVGQYSEHTAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKRLTSLHGSIE 549
 Qy 543 NLIYDPEQNDHEHGLDORSKPIILFSMARLDRVKNITGLVEAFKAKRLRLNVLVVAG 602
 Db 550 ELLYSTVNEEHI CVLNDRSKPIILFTMARLDRVKNITGLVEAFKAKRLRLNVLVVAG 609
 Qy 603 YNDVNSKDRBEIAIEKQHELIKTHNLFGQFRWISAOQTNBARNGELYRIADTHGAFVQ 662
 Db 610 -DRRKESKDLFEKAEKMKYELIETIKNGQFRWISSQMNVRNGELYRIADTHGAFVQ 668
 Qy 663 PALYEAFGLTWVEAMTGLPTFATLHGSPABII EHGVSFGPHIDVPHQOAVNLMDPDR 722
 Db 669 PAFYEAFGLTWVEAMTGLPTFATLHGSPABII EHGVSFGPHIDVPHQOAVNLMDPDR 728
 Qy 723 CKQDPDHWNVISGAGLQRIYKTYKILYSERLMTLAGYGVFKVSKLERLETTRYLEM 782
 Db 729 CKQPSHWETISGGLAKRIQEKYTWQIYSERLLTLLAAVYGVFKVSKLERLETTRYLEM 788
 Qy 783 YILKRELAKTVPLAID 799
 Db 789 YALKYRWMAEAVPLAAE 805

RESULT 15

SUSU_VICFA STANDARD; PRT; 806 AA.
 AC P31926;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sucrose synthase [EC 2.4.1.13] (Sucrose-UDP glucosyltransferase).
 GN SUCS.
 OS *Vicia faba* (Broad bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Papilionoideae; Viciaeae; Vicia.
 OX NCBI_TaxID=3906;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Fzibo;
 RX MEDLINE=93379571; PubMed=7764025;
 RA Heim U., Weber H., Baumein H., Wobus U.;
 RA "A sucrose-synthase gene of *Vicia faba* L.: expression pattern in
 RT developing seeds in relation to starch synthesis and metabolic
 RT regulation.";
 RL Planta 191:394-401(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Kleine Thueringer; TISSUE=Root nodules;
 RX MEDLINE=94003420; PubMed=8430379;
 RA Kuster H., Fruhling M., Perlick A.M., Puchler A.;
 RA "The sucrose synthase gene is predominantly expressed in the root
 RT nodule tissue of *Vicia faba*.";

RL Mol. Plant Microbe Interact. 6:507-514(1993).
 CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
 CC fructose for various metabolic pathways.
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
 CC -!- SIMILARITY: Belongs to the glucosyltransferase family 1. Plant
 CC sucrose synthase subfamily.
 CC
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 CC
 CC EMBL; X69773; CAA49428.1; -;
 CC EMBL; M97551; AAC37346.1; -;
 CC PIR; S31479; S31479.
 CC InterPro; IPR001296; Glyco_trans_1.
 CC InterPro; IPR000368; Sucrose synth.
 CC Pfam; PF00534; Glycos_transf_1; 1.
 CC Pfam; PF00862; Sucrose synth; 1.
 CC Transferrase; Glycosyltransferase.
 CC KW
 CC SEQUENCE 806 AA; 92520 MW; A54B004C0732F306 CRC64;

Query Match 69.8%; Score 2944.5; DB 1; Length 806;

Best Local Similarity 68.8%; Pred. No. 1.8e-188;

Matches 549; Conservative 122; Mismatches 126; Indels 1; Gaps 1;

Qy 3 HASGDRVEDTHAHRNELVALLSKYVKNKGILQPHILDLALDEVGSGGRALAEGLFD 62
 Db 10 HSLRLELDITANRNEITALLSRIEAKGKILQHQHVIAPETPEENRQKLTGATGE 69
 Qy 63 VLRSQAENIVLPFVAVATVRPRPGVWEYVRVNVHELVSQILTVSEYLFKELVDQND 122
 Db 70 VLRSQAENIVLPFVAVATVRPRPGVWEYLRVNVHALVVENLQPAEFLKELVDGSANG 129
 Qy 123 PYVLELOFEPNVSPVRPNRSSISNGVQFNLRHLSSIMFRNDCLEPLDLFLGRHRKG 182
 Db 130 NFVLELOFEPNVSPVRPNRSSISNGVQFNLRHLSSIMFRNDCLEPLDLFLGRHRKG 189
 Qy 183 HVMLNDRIQSLGRLOSVLTAKAEHLSKLPADTPYSQFAYKFOEWGLEKMGDTHAGVLE 242
 Db 190 KTMINDRIQNPDSILQHVLRKAEVLTSTVDPTPYSEEFHFEHFEHFEHFEHFEHFEH 249
 Qy 243 MIHLLLDIIQAPDSTLEKFLGRIPMLFNVVVSPHSGYFGQANVLGPDGTGGQIVYILDQ 302
 Db 250 SIQLELDLEAPDSTLEKFLGRIPMLFNVVVSPHSGYFGQANVLGPDGTGGQIVYILDQ 309
 Qy 303 VRALENEMWRLKKGGLDVSFKILIVRLIPDAGTSCNORLERISGTOHTYILRVFERN 362
 Db 310 VRALENEMWRLKKGGLDVSFKILIVRLIPDAGTSCNORLERISGTOHTYILRVFERN 369
 Qy 363 ENGLKWKWISRFDPWVPLETFAEDAAGEIAAELQCTPDIIGNYSDGNLVAISLKYKGI 422
 Db 370 EKGIVRWISRFEPWVPLETFAEDAAGEIAAELQCTPDIIGNYSDGNLVAISLKYKGI 429
 Qy 423 TQCMIAHALEKTKYPDSDI FWNKDEKXHFSCQPTADIIAMNADFIITSTYQBIAGSKN 482
 Db 430 TQCTIAHALEKTKYPDSDI FWNKDEKXHFSCQPTADIIAMNADFIITSTYQBIAGSKN 489
 Qy 483 TVGQYSEHTAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKRLTSLHGSIE 542
 Db 490 TVGQYSEHTAFTLPGILRVVHGIDVDPKFNIVSPGADMSIYFPHTKAKRLTSLHGSIE 549
 Qy 543 NLIYDPEQNDHEHGLDORSKPIILFSMARLDRVKNITGLVEAFKAKRLRLNVLVVAG 602
 Db 550 ELLYSTVNEEHI CVLNDRSKPIILFTMARLDRVKNITGLVEAFKAKRLRLNVLVVAG 609
 Qy 603 YNDVNSKDRBEIAIEKQHELIKTHNLFGQFRWISAOQTNBARNGELYRIADTHGAFVQ 662
 Db 610 -DRRKESKDLFEKAEKMKYELIETIKNGQFRWISSQMNVRNGELYRIADTHGAFVQ 668

QY	663	PALYEPGLTVVEAMTCGLPTEATLHGCPAEIIEHGVSGFHIDPYHPQAVNLMADEFR	722
Db	669	PAVEAFGLTVVEAMATGLPTEATLHGCPAEIIVHGKSGFHIDPYHGRADLLVEFEK	728
QY	723	CKQDPDHWNNISGAGLQRIYKYTWKIYSERLMTLAGVYGFVKYVSKLERLETRRYLEMF	782
Db	729	VKADPSEHDKISLGLQRIEKEYTWQIYSORLLTLTGTVYGFVKHVSNDRLSRRYLEMF	788
QY	783	YILKPRELAKTVPLAIDQ	800
Db	789	YALKYRXLAESVPLAVEE	806

Search completed: May 24, 2004, 11:27:59
Job time : 16.9392 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:38 ; Search time 40.8218 Seconds
(without alignments)
6198.778 Million cell updates/sec

Title: US-10-080-114A-2

Perfect score: 4217

Sequence: 1 STHASGRVDTLHARNEL.....YILKRELAKTVLAIDQPQ 802

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1217041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4186	99.3	796	10	Q93WS3 zea mays (m
2	4178	99.1	809	10	Q8L5H0
3	3523	83.5	811	10	Q9SLY2 citrus unsh
4	3506	83.1	811	10	Q9SLV8 citrus unsh
5	3456	82.0	809	10	Q9ML11 arabidopsis
6	3396	80.5	812	10	Q9FRX3 pyrus pyrif
7	3377	80.1	811	10	Q84T18 solanum tub
8	3366	79.8	808	10	Q9SBD5 arabidopsis
9	3297	78.2	822	10	Q94G60 beta vulgar
10	3263	77.4	811	10	Q9ZPC5 cratogeomys
11	3117	73.9	809	10	Q9ZPC6 cratogeomys
12	2998.5	71.1	806	10	Q9SBL8 citrus unsh
13	2991	70.9	816	10	Q8W1W4 bambusa old
14	2984.5	70.8	805	10	Q9SL52 citrus unsh
15	2982.5	70.7	808	10	Q8W1W3 bambusa old
16	2982	70.7	816	10	Q43706 zea mays (m

17	2968.5	70.4	805	10	Q9SLY1 citrus unsh
18	2968.5	70.4	808	10	Q8W1W2 bambusa old
19	2967.5	70.4	802	10	Q9LKR0 saccharum o
20	2961	70.2	806	10	Q9XGB7 gossypium h
21	2958	70.1	816	10	Q8LJT5 oncidium cv
22	2954	70.0	816	10	Q8LJT4 x mokara cv
23	2953	70.0	816	10	Q8GS23 oryza sativ
24	2944.5	69.8	805	10	Q7Y078 solanum tub
25	2943.5	69.8	805	10	Q82693 lycopersico
26	2943.5	69.8	806	10	Q9TOM9 pisum sativ
27	2937.5	69.7	804	10	Q9AVR8 pisum sativ
28	2936.5	69.6	806	10	Q81610 medicago tr
29	2934.5	69.6	805	10	Q9TOM6 medicago tr
30	2933.5	69.6	815	10	Q43223 triticum ae
31	2929.5	69.5	803	10	Q9LW57 chenopodium
32	2925.5	69.4	805	10	Q9XG65 medicago tr
33	2924.5	69.4	805	10	Q8GTAC3 phaseolus v
34	2919.5	69.2	805	10	Q84UC3 solanum tub
35	2913.5	69.1	805	10	Q82691 lycopersico
36	2904.5	68.9	808	10	Q9LXL5 arabidopsis
37	2892.5	68.6	808	10	Q82073 triticum ae
38	2340.5	55.5	942	10	Q9FX32 arabidopsis
39	2310.5	54.8	887	10	Q9FHU4 arabidopsis
40	2259.5	53.6	798	10	Q7XNX5 oryza sativ
41	2251.5	53.4	798	10	Q7XXL1 oryza sativ
42	2125	50.4	794	16	Q820M5 nitrosomona
43	2093.5	49.6	532	10	Q94CC8 arabidopsis
44	1841.5	43.7	808	16	Q8DK23 synechococc
45	1833	43.5	806	2	Q9ZEV2 anabaena sp

ALIGNMENTS

RESULT 1					
Q93WS3					
ID	Q93WS3	PRELIMINARY;	PRT;	796 AA.	
AC	Q93WS3;				
DT	01-DEC-2001 (TRENBLrel. 19, Created)				
DT	01-DEC-2001 (TRENBLrel. 19, Last sequence update)				
DT	01-JUN-2003 (TRENBLrel. 24, Last annotation update)				
DE	Sucrose synthase (Fragment).				
OS	Zea mays (Maize).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.				
OX	NCBI_TaxID=4577;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Root;				
RA	Carlson S.J., Chourey P.S., Helentjaris T., Datta R.;				
RT	"Gene expression studies on developing kernels of maize sucrose synthase (SuSy) mutants show evidence for a third SuSy gene."				
RL	Plant Mol. Biol. 0:0-0(2001).				
DR	EMBL; AY059416; AAL27096.1; -				
DR	GO; GO:0009058; P:biosynthesis; IEA.				
DR	GO; GO:0005985; P:sucrose metabolism; IEA.				
DR	InterPro; IPR001296; Glyco_transf.1.				
DR	InterPro; IPR00368; Sucrose_synth.				
DR	Pfam; PF00534; Glycos_transf.1; 1.				
DR	Pfam; PF00862; Sucrose_synth; 1.				
FT	NON_TER				
SQ	SEQUENCE 796 AA; 90453 MW; 7E7A92CB0C31F898 CRC64;				
Query Match	99.3%;	Score	4186;	DB	10; Length 796;
Best Local Similarity	100.0%;	Pred. No.	1.2e-300;		
Matches	796;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
QY	7	DEVEDTLHARNELVALLSKYVNGKGLIOPHHILDALDEVCGSGERALAEGPFLDLVLS	66		
DB	1	DEVEDTLHARNELVALLSKYVNGKGLIOPHHILDALDEVCGSGERALAEGPFLDLVLS	60		
QY	67	AQEIVLPPFVAIAVRPRPGWWEYVRVNVNHELVSQTLVSEYLRFRKEELVDGQNDPPYL	126		

Db 61 AQAELVLPFFVAIAVRPGVWEYVRVNVHLSVEQLTVSEYLRFAKELVDGQNDPYVL 120
 QY 127 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDRCLDLEPLDFLRGRHHRKHGVM 186
 Db 121 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDRCLDLEPLDFLRGRHHRKHGVM 180
 QY 187 LNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 246
 Db 181 LNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 240
 QY 247 LLDIIQAPDPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 306
 Db 241 LLDIIQAPDPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 300
 QY 307 ENEMVLRLKKQGLDVSFKLIVTRLPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 366
 Db 301 ENEMVLRLKKQGLDVSFKLIVTRLPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 360
 QY 367 LKKNISRPDVPWVLETFARDAAGEIAAELOQTPDFIIGNYSQNLVASLLSYKMGITQCN 426
 Db 361 LKKNISRPDVPWVLETFARDAAGEIAAELOQTPDFIIGNYSQNLVASLLSYKMGITQCN 420
 QY 427 IAHALEKTYPDSDFWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 486
 Db 421 IAHALEKTYPDSDFWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 480
 QY 487 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSINLIY 546
 Db 481 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSINLIY 540
 QY 547 DPEONDEHGHLDLDRSKPILFMSARLDVRKNITGLVEAFKAKKAKRELNVLVVAGYNDV 606
 Db 541 DPEONDEHGHLDLDRSKPILFMSARLDVRKNITGLVEAFKAKKAKRELNVLVVAGYNDV 600
 QY 607 NKSQKREIEAEIEKMHLEIKTNLFQGFWMISQATNRANGELYRYIADTHGAFVQPALY 666
 Db 601 NKSQKREIEAEIEKMHLEIKTNLFQGFWMISQATNRANGELYRYIADTHGAFVQPALY 660
 QY 667 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDYPHPQAVNLMADFFDRCKQD 726
 Db 661 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDYPHPQAVNLMADFFDRCKQD 720
 QY 727 PDHWNISAGLQRIYKTYKWTYKYSRLMTLAGYGVGFWKYSKLERLETTRYLEMFIYK 786
 Db 721 PDHWNISAGLQRIYKTYKWTYKYSRLMTLAGYGVGFWKYSKLERLETTRYLEMFIYK 780
 QY 787 FRELAKTVPLAIDQPO 802
 Db 781 FRELAKTVPLAIDQPO 796

RESULT 2
 Q8L5H0 PRELIMINARY; PRT; 809 AA.
 ID Q8L5H0
 AC Q8L5H0
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Sucrose synthase 3 (EC 2.4.1.13).
 CS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 CX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=cv. Caramba; TISSUE=Anaerobic root;
 RA Holtgraeve J.L., Scholz A., Altmann B., Winter H.;
 RT "Complete coding sequence of a third sucrose synthase isoform in
 maize."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY124703; AA:M89473.1; -

DR GO: 0016157; P:sucrose synthase activity; IEA.
 DR GO: 0016757; P:transferase activity, transferring glycosyl...; IEA.
 DR GO: 0009056; P:biosynthesis; IEA.
 DR GO: 0005985; P:sucrose metabolism; IEA.
 DR InterPro: IPR001296; Glyco trans 1.
 DR InterPro: IPR00368; Sucrose synth.
 DR Pfam: PF00534; Glycos transf 1; 1.
 DR Pfam: PF00862; Sucrose synth; 1.
 DR Transferase; Glycosyltransferase.
 KW

SQ SEQUENCE 809 AA; 31926 MW; 848FA01AD3CC6C19 CRC64;
 Query Match 99.1%; Score 4176; DB 10; Length 809;
 Best Local Similarity 99.7%; Pred. No. 4.7e-300;
 Matches 794; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 DRVEDTLAHRNELVALLSKYVNGKGILOPHHILDALDEVQSGGRALAEGLDVLRS 66
 Db 14 DRVEDTLAHRNELVALLSKYVNGKGILOPHHILDALDEVQSGGRALAEGLDVLRS 73
 QY 67 AQEAIVLPPFVAIAVRPGVWEYVRVNVHLSVEQLTVSEYLRFAKELVDGQNDPYVL 126
 Db 74 AQEAIVLPPFVAIAVRPGVWEYVRVNVHLSVEQLTVSEYLRFAKELVDGQNDPYVL 133
 QY 127 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDRCLDLEPLDFLRGRHHRKHGVM 186
 Db 134 ELDFEPFNVSPRPNRSSISGVQVFLNRHLSIMFRNDRCLDLEPLDFLRGRHHRKHGVM 193
 QY 187 LNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 246
 Db 194 LNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEWGLEKGGWGTAGHVLMIHL 253
 QY 247 LLDIIQAPDPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 306
 Db 254 LLDIIQAPDPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVVILDOVRAL 313
 QY 307 ENEMVLRLKKQGLDVSFKLIVTRLPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 366
 Db 314 ENEMVLRLKKQGLDVSFKLIVTRLPDAKGTSCNQLERISGTQHTYILRVFPFRNENGI 373
 QY 367 LKKNISRPDVPWVLETFARDAAGEIAAELOQTPDFIIGNYSQNLVASLLSYKMGITQCN 426
 Db 374 LKKNISRPDVPWVLETFARDAAGEIAAELOQTPDFIIGNYSQNLVASLLSYKMGITQCN 433
 QY 427 IAHALEKTYPDSDFWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 486
 Db 434 IAHALEKTYPDSDFWKNFDEKYPHSCQFTADIAMNNADFIITSTYQEIAGSKNTVQ 493
 QY 487 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSINLIY 546
 Db 494 YESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSINLIY 553
 QY 547 DPEONDEHGHLDLDRSKPILFMSARLDVRKNITGLVEAFKAKKAKRELNVLVVAGYNDV 606
 Db 554 DPEONDEHGHLDLDRSKPILFMSARLDVRKNITGLVEAFKAKKAKRELNVLVVAGYNDV 613
 QY 607 NKSQKREIEAEIEKMHLEIKTNLFQGFWMISQATNRANGELYRYIADTHGAFVQPALY 666
 Db 614 NKSQKREIEAEIEKMHLEIKTNLFQGFWMISQATNRANGELYRYIADTHGAFVQPALY 673
 QY 667 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDYPHPQAVNLMADFFDRCKQD 726
 Db 674 EAFGLTVVEAMTCGLPTFATLHGGPAEIEHGVSGFHIDYPHPQAVNLMADFFDRCKQD 733
 QY 727 PDHWNISAGLQRIYKTYKWTYKYSRLMTLAGYGVGFWKYSKLERLETTRYLEMFIYK 786
 Db 734 PDHWNISAGLQRIYKTYKWTYKYSRLMTLAGYGVGFWKYSKLERLETTRYLEMFIYK 793
 QY 787 FRELAKTVPLAIDQPO 802
 Db 794 FRELAKTVPLAIDQPO 809

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Q9SLY2 PRELIMINARY; PRT; 811 AA.
ID Q9SLY2
AC Q9SLY2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update);
DE Sucrose synthase.
GN CITRUS.
OS Citrus unshiu (satsuma orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=55188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Miyagawa-Wase; TISSUE=fruit;
RA Komatsu A.;
RT "Isolation of three sucrose synthase isoforms from Citrus.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB022091; BAA88904.1; -.
DR GO; GO:0009058; P:biomethylation; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos_trans_1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
SQ SEQUENCE 811 AA; 92633 MW; 0682BAF7AAAB58F0 CRC64;

Query Match 83.5%; Score 3523; DB 10; Length 811;
Best Local Similarity 82.6%; Pred. No. 1.4e-251;
Matches 655; Conservative 70; Mismatches 66; Indels 2; Gaps 1;

QY 7 DRVEDTLFAHNEALVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 64
DB 14 ERVEDTLVHNEALVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 73
QY 65 RSAQEAIVLPFFVAIAVRPRGWEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 124
DB 74 KSAQEAIVLPFFVAIAVRPRGWEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 133
QY 125 VLELDFPFPNVSPRPNRSSISGNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 184
DB 134 VLELDFPFPNVSPRPNRSSISGNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 193
QY 185 MMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFEWGLEKMGDTAGHVLMI 244
DB 194 LMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFEWGLEKMGDTAGHVLMI 253
QY 245 HLLDIIQADPPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 304
DB 254 HLLDIIQADPPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 313
QY 305 ALENEMVLRLKQGLDVSPKILIVTRLPDAKGTSCNQLERISGTOHTYILRVPPREN 364
DB 314 ALENEMVLRLKQGLDVSPKILIVTRLPDAKGTSCNQLERISGTOHTYILRVPPREN 373
QY 365 GILKKWISRFDPVWPYLETFAEDAAGEIAAELQGTDFIIGNYSDGNLVSLLSYKMGITQ 424
DB 374 GILKKWISRFDPVWPYLETFAEDAAGEIAAELQGTDFIIGNYSDGNLVSLLSYKMGITQ 433
QY 425 CNIAHALEKTKYPSDIIENKFNDEKHYSCFTADIIANNADFTITSTYQEIAGSKNTV 484
DB 434 CNIAHALEKTKYPSDIIENKFNDEKHYSCFTADIIANNADFTITSTYQEIAGSKNTV 493
QY 485 QYESHSTAFTLPGLRVVVGIDVDPKENVISPGADMSIYFPHTEKAKRLTSLHGSIEHL 544
DB 494 QYESHSTAFTLPGLRVVVGIDVDPKENVISPGADMSIYFPHTEKAKRLTSLHGSIEHL 553
QY 545 TYDEQNDHEHTGLDSDRSPKILFMSMARLDVYKNTGLVEAFKAKRELNVLVVAGYN 604
DB 554 LFDPEQNDHEHTGLDSDRSPKILFMSMARLDVYKNTGLVEAFKAKRELNVLVVAGYN 613
QY 605 DVNKSQDREETAIEKMHLEIKTNLRFQPRWISAQTRNARNGELRYRIADTHGAFVQPA 664

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DB 614 DVNKSQDREETAIEKMHLEIKTNLRFQPRWISAQTRNARNGELRYRIADTHGAFVQPA 673
QY 665 LYEAFLGTVVEAMTCGLPTFATLHGSPAEIIIEHGVSGPHIDPYPEQAVNLMADFPDRCK 724
DB 674 FYEAFGLTVVEAMTCGLPTFATLHGSPAEIIIEHGVSGPHIDPYPEQAVNLMADFPDRCK 733
QY 725 QDPDHWNISGAGIQRIVYKWTWKIYSERLMTLAGVYGFVYVSKLETERRYLEMFYI 784
DB 734 ENPSHWKKISDGGUKRIYRIYTWIKIYSERLMTLAGVYGFVYVSKLETERRYLEMFYI 793
QY 785 LKPRELAKTVPLA 797
DB 794 LKFRDLVKSUPLA 806

RESULT 4
Q9SLV8 PRELIMINARY; PRT; 811 AA.
ID Q9SLV8
AC Q9SLV8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update);
DE Sucrose synthase.
GN CITRUS-2.
OS Citrus unshiu (satsuma orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=55188;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu A.;
RT "Cloning of sucrose synthase (CITSUSA) gene from Citrus.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025778; BAA88981.1; -.
DR GO; GO:0009058; P:biomethylation; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos_trans_1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
SQ SEQUENCE 811 AA; 92549 MW; E7868C77BD1ELB3E CRC64;

Query Match 83.1%; Score 3506; DB 10; Length 811;
Best Local Similarity 82.1%; Pred. No. 2.5e-250;
Matches 651; Conservative 72; Mismatches 68; Indels 2; Gaps 1;

QY 7 DRVEDTLFAHNEALVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 64
DB 14 ERVEDTLVHNEALVALLSKYVNGKGILOPHHILDALDEVQ--SGGRALAEGLFDVL 73
QY 65 RSAQEAIVLPFFVAIAVRPRGWEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 124
DB 74 KSAQEAIVLPFFVAIAVRPRGWEYVNVVHLSVQLTVSEYLRKKEELVDQNDPY 133
QY 125 VLELDFPFPNVSPRPNRSSISGNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 184
DB 134 VLELDFPFPNVSPRPNRSSISGNGVQFLNRHLSIMFRNRDCLPELDFLRGHRKHGV 193
QY 185 MMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFEWGLEKMGDTAGHVLMI 244
DB 194 LMLNDRIQSLGRQLSVLTAKAEHLKSLPADTPYSQFAYKFEWGLEKMGDTAGHVLMI 253
QY 245 HLLDIIQADPPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 304
DB 254 HLLDIIQADPPSTLEKFLGRIPMIENNVVSPHGYFGQANVLGLPDTGGQIVYLDQVR 313
QY 305 ALENEMVLRLKQGLDVSPKILIVTRLPDAKGTSCNQLERISGTOHTYILRVPPREN 364
DB 314 ALENEMVLRLKQGLDVSPKILIVTRLPDAKGTSCNQLERISGTOHTYILRVPPREN 373
QY 365 GILKKWISRFDPVWPYLETFAEDAAGEIAAELQGTDFIIGNYSDGNLVSLLSYKMGITQ 424

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QY 605 DVNKSXDRREIAEIEBKWEHLIKTNLFGQFRWISAOQNRARNGBLYRYIADTHGAFVQPA 664
Db 614 DVNKSXDRREIEIEBKWEHLIKTNLFGQFRWISAOQNRARNGBLYRYIADTHGAFVQPA 673
QY 665 LYEAAGLTUVVEAMTCGLPTATLHGSPAEIIEHGVSGFHDIPYHPQAVNLMDPFFORCK 724
Db 674 FYEAFGLTVVEAMTCGLPTATLHGSPAEIIEHGVSGFHDIPYHPQAVNLMDPFFORCK 733
QY 725 QDPDHWNNISGAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 784
Db 734 EDNHNKKVSDAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 793
QY 785 LKFRDLAKTVPLAID 799
Db 794 LKFRDLAKTVPEAD 808

RESULT 6
Q9FRX3 PRELIMINARY; PRT; 812 AA.
AC Q9FRX3;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Sucrose synthase 1.
GN PYRUS1.
OS Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Rosales; Rosaceae; Maloideae; Pyrus.
OX NCBI_TaxID=3767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Hosui; TISSUE=Fruit flesh;
RA Tanase K., Shiratake K., Mori H., Yamaki S.;
RT "Cloning and expression of SUS genes with development of Japanese pear
RT fruit.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045710; BAB20799.1; -.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco.trans.1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos.transf.1; 1.
DR Pfam; PF00862; Sucrose synth. 1.
SQ SEQUENCE 812 AA; 93079 MW; 8F9A26C08:E541B4 CRC64;

Query Match 80.5%; Score 3396; DB 10; Length 812;
Best Local Similarity 79.6%; Pred. No. 3.4e-242;
Matches 633; Conservative 84; Mismatches 76; Indels 2; Gaps 1;

QY 7 DRVEDTLHARNELVALLSKYVNGKGILOPHHLDALDEVQ--SGGRALAEQPFLLDYL 64
Db 15 ERVEDTLSDHRELVALLSRVLDQCKRILOPHHLDLDQIIVIGDDEAKQKNGPFSEVL 74

QY 65 RSAQAIVLPPVAJAVPRPGVWEYVRVNVNHELHVEQLTVSEYLRPKHELVDGQNDPY 124
Db 75 KSAQAIVLPPYVALAVPRPGVWDYVRVNVYELHVEQLTVSEYLRPKHELVDGESSDKY 134

QY 125 VLELDFEFPNVSPRPNSSSGNGVOFLNRHLSSSTMPFNRCPLDPLFLGRHKGHV 184
Db 135 VLELDFEFPNAPPRPTSSSGNGVOFLNRHLSSSTMPFNRCPLDPLFLGRHKGHV 194

QY 185 MMLNDRIQSLGRLVTKAEHSLKPADTPYSQFAYKFOEGKLGWGTAGHYLEMI 244
Db 135 LMLNDRIQSVSKLQALAKAEHSLKQEPETYSSEYLFQKMGFGRGWDATVHVLEMM 254

QY 245 HLLLDIIQAPDPTLEKFLGRIPMIPNVVSVPHGVFGQANVLGLPDTGGQIYILDQVR 304
Db 255 HLLLDIIQAPDPTLEKFLGRIPMIPNVVSVPHGVFGQANVLGLPDTGGQIYILDQVR 314

QY 305 ALENEMVLEKKQGLDVSFKIILVTLIPDAKGTSCNQLRISGTOHTYIILRVPRNEN 364

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Db 315 ALEKEMLERIRKQGLDFTPRLLIVTRLIPEAKGITCNQRLREISGTEHTHILRVPERSEK 374
QY 365 GILKKWISRPDVWPLETFAEDAAGEIAAEIQTGPDFFIIGNYSDGNLVASLLSYKMGITQ 424
Db 375 GILKKWISRPDVWPLETFAEDAAGEIAAEIQTGPDFFIIGNYSDGNLVASLLSYKMGITQ 434
QY 425 CNIAHALEKTYPPSDIPFWKPFDESKYHESCOPTADIIAMNADFIITSTYQBIAGSKNTV 484
Db 435 CTIAHALEKTYPPSDIYWKKEFEHEHSTQFTADLIAMNADFIITSTYQBIAGTKDFV 494
QY 485 QOYESHTAFTLPGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTPKAKRLTSLHSGIEML 544
Db 495 QOYESHSSYTLPGQYRVVHGINVDPKFNIVSPGADMTIYPPSEKQRLTSLHSGIEML 554
QY 545 IYDPEQNDHGHLDHRSKPIFLSMARLDRVKNITGLVEAFKAKAKRELNVNVVAGVN 604
Db 555 LYNPDQNDVHIGTILSDRSKPIIFSMARLDQVKMTGLVECYAKAKSKLRLDLANLVIVAGYI 614
QY 605 DVNKSXDRREIAEIEBKWEHLIKTNLFGQFRWISAOQNRARNGBLYRYIADTHGAFVQPA 664
Db 615 DVNKSXDRREIAEIEBKWEHLIKTNLFGQFRWISAOQNRARNGBLYRYIADTHGAFVQPA 674
QY 665 LYEAAGLTUVVEAMTCGLPTATLHGSPAEIIEHGVSGFHDIPYHPQAVNLMDPFFORCK 724
Db 675 FYEAFGLTVVEAMTCGLPTATLHGSPAEIIEHGVSGFHDIPYHPQAVNLMDPFFORCK 734
QY 725 QDPDHWNNISGAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 784
Db 735 EDNHNKKVSDAGLQRIYKYTWKIYSERLMTLAGVYGFNKKVSKLERLETRRYLEMFYI 794
QY 785 LKFRDLAKTVPLAID 799
Db 795 LKFRDLAKTVPEAD 809

RESULT 7
Q94T18 PRELIMINARY; PRT; 811 AA.
AC Q94T18;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Sucrose synthase.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree;
RA Loureiro M., Kopka J., Mueller-Roeber B., Trethewey R.;
RT "Characterization of effects of specific reduction in gene expression
RT of two sucrose synthase genes in transgenic potato plants.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY205302; AAO67719.1; -.
DR GO; GO:0005958; P:biogenesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco.trans.1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos.transf.1; 1.
DR Pfam; PF00862; Sucrose synth. 1.
SQ SEQUENCE 811 AA; 92775 MW; F4C99F1C862DD535 CRC64;

Query Match 80.1%; Score 3377; DB 10; Length 811;
Best Local Similarity 78.9%; Pred. No. 8.7e-241;
Matches 627; Conservative 84; Mismatches 82; Indels 2; Gaps 1;

QY 7 DRVEDTLHARNELVALLSKYVNGKGILOPHHLDALDEV--QSGGRALAEQPFLLDYL 64
Db 14 ERVEDTLHARNELVALLSKYVNGKGILOPHHLDALDEFNSAVCDTACEKLEKSGPFCEIL 73

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Qy	65	RS	Q	A	E	A	I	V	L	P	P	F	V	A	I	A	V	R	P	G	V	W	E	Y	V	R	V	N	W	E	Y	S	V	Q	L	T	V	S	E	Y	L	R	P	K	B	E	L	V	D	G	H	N	D	P	Y	124		
Db	74	K	S	T	Q	E	A	I	V	L	P	P	F	V	A	I	A	V	R	P	G	V	W	E	Y	V	R	V	N	W	E	Y	S	V	Q	L	T	V	S	E	Y	L	R	P	K	B	E	L	V	D	G	E	N	N	L	F	133	
Qy	125	V	L	E	D	P	F	P	F	N	V	S	U	P	R	P	R	S	S	I	G	N	G	V	O	F	L	N	P	H	L	S	I	M	F	R	N	E	D	C	L	E	P	L	D	P	L	R	G	H	R	H	K	G	V	184		
Db	134	V	L	E	D	P	F	P	F	N	V	S	U	P	R	P	R	S	S	I	G	N	G	V	O	F	L	N	P	H	L	S	N	M	F	R	S	K	E	S	D	P	L	D	P	L	R	G	H	R	H	K	G	V	193			
Qy	185	M	L	M	N	D	R	I	Q	S	L	R	O	S	V	I	T	K	A	B	E	H	L	S	K	L	P	A	D	T	P	Y	S	Q	F	A	K	E	Q	E	W	G	L	E	K	O	G	D	T	A	G	V	L	E	M	I	244	
Db	194	L	M	L	N	E	R	I	Q	R	I	S	E	L	S	S	L	N	K	A	D	D	Y	L	S	K	L	P	T	P	T	Y	T	E	F	E	V	A	L	Q	E	M	F	E	K	O	G	D	T	A	K	R	V	L	E	M	I	253
Qy	245	H	L	L	D	I	I	Q	A	P	D	S	T	L	E	F	L	G	R	P	M	E	F	N	V	V	V	S	P	R	G	Y	F	Q	O	A	N	V	L	G	L	D	P	T	G	G	O	V	I	L	D	O	V	R	304			
Db	254	H	L	L	S	D	I	L	Q	A	P	D	S	T	L	E	F	L	G	R	P	M	E	F	N	V	V	V	S	P	R	G	Y	F	Q	O	A	N	V	L	G	L	D	P	T	G	G	O	V	I	L	D	O	V	R	313		
Qy	305	A	L	E	N	E	M	L	R	I	K	O	G	L	D	V	S	P	K	I	L	I	V	T	R	L	P	D	A	K	G	N	S	C	N	O	R	L	E	R	I	S	T	O	C	H	T	Y	L	I	R	V	P	F	R	E	N	364
Db	314	A	L	E	A	E	M	L	R	I	K	O	G	L	N	F	K	P	K	I	L	I	V	T	R	L	P	D	A	K	G	I	T	C	N	O	R	L	E	R	I	S	T	E	S	H	I	L	R	V	P	F	R	E	N	373		
Qy	365	G	I	L	K	W	I	S	R	F	D	V	P	Y	L	E	F	A	E	D	A	G	E	I	A	A	E	L	Q	G	T	P	D	F	I	I	G	N	S	D	G	N	L	V	A	S	L	I	S	R	G	M	G	I	T	O	424	
Db	374	G	I	L	K	W	I	S	R	F	D	V	P	Y	L	E	F	A	E	D	V	A	G	E	M	S	A	E	L	Q	G	V	E	D	L	I	I	G	N	S	D	G	N	L	V	A	S	L	I	A	K	W	G	V	T	O	433	
Qy	425	C	N	I	A	H	E	K	T	Y	P	S	D	I	F	W	K	N	P	D	E	K	H	S	C	O	P	T	A	D	I	I	A	M	N	A	D	P	I	T	T	Y	Q	B	I	A	G	S	K	N	T	V	484					
Db	434	C	T	I	A	H	E	K	T	Y	P	S	D	I	F	W	K	N	P	E	B	E	K	H	S	C	O	P	T	A	D	L	L	S</																								

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RESULT 8
Q9SBD5
Q9SBD5 PRELIMINARY; PRT; 808 AA.
ID Q9SBD5
AC Q9SBD5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE T2H3 .8 protein.
DE T2H3 .8
GN Arabidopsis thaliana (Mouse-ear cress) .
OS Arabidopsis thaliana (Mouse-ear cress) .
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis .
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Wastu;
RL "The A. thaliana Genome Sequencing Project.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

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[illegible]

QY 725 QDPDHWNTSGAGLQRIYKTYWIKYISERLMTLAGVYGFYKYSKLERLETRRYLEMFYI 784
Db 722 EDNHNKVKSDAGLQRIYERYTWIKYISERLMTLAGVYGFYKYSKLERLETRRYLEMFYI 781
QY 785 LKPEREL 790
Db 782 LKPRDL 787
RESULT 9
Q94G60 PRELIMINARY; PRT; 822 AA.
AC Q94G60;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13).
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Beta.
OX NCBI_TaxID=161934;
RN [1]
RP SEQUENCE FROM N.A.
RA Witt I., Basner A., Willmitzer L., Hoefgen R., Hesse H.;
RT "Genomic copy of Sucrose synthase from sugar Beet.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF273253; AAK65960.1; -.
DR GO; GO:0016157; F:sucrose synthase activity; IEA.
DR GO; GO:0016757; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR InterPro; IPR00368; Sucrose synth.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00862; Sucrose synth_1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 822 AA; 93660 MW; 009BE481613DAC7 CRC64;
Query Match 78.2%; Score 3297; DB 10; Length 822;
Best Local Similarity 78.2%; Pred. No. 7.4e-235;
Matches 623; Conservative 80; Mismatches 90; Indels 4; Gaps 3;
QY 7 DRVEDTLAHNRNELVALLSKYVKNKGLIQPHHLDALDFVQ--SGGRALAGPFLDVL 64
Db 13 ERVEDTLVSRHRELVSLSKYVAQKCLQPHHLDGLSVIGEDKGOILSDGPFSEVL 72
QY 65 RSAQEAIVLPFVAIVAPRPGWVEYVRVNVHLSVEQLTVSEYLRPKBELVDGQNDPY 124
Db 73 RSAQEAIVLPFVAIVAPRPGWVEYVRVNVHLSVEQLTVSEYLRPKBELVDGKADHY 132
QY 125 VLEIDFPFNVSPRPNRSSIGNGVQVFLNRHLSIMFRNDCLEPLDLFLRHHKGVH 184
Db 133 VLEIDFPFNVSPRPNRSSIGNGVQVFLNRHLSIMFRNDCLEPLDLFLRHHKGVV 192
QY 185 MMLNDRLQSLQSLVTKAEHLKSLPADPYSOFAKFOEWGLKMGOTAGHVLMI 244
Db 193 MMLNDRIQTIQRLQSLAKAEHYLKLKPADPYSEFEVIQMGFPERGWDIAERVLEMM 252
QY 245 HLLLDILQAPDPSTLEKFLGRIPMIFNVVSPHGYFGQANVLGPDTCGQIVYILDQVR 304
Db 253 HLLLDILQAPDPSTLEKFLGRIPMIFNVVSPHGYFGQANVLGPDTCGQIVYILDQVR 312
QY 305 ALENEMVLRKXQGLDVPKILIVTRLPDAKGTSCNQLERISGTMTYILRVFRNEN 364
Db 313 SLEREMVLRKXQGLDVPKILIVTRLPDAKGTSCNQLERISGTMTYILRVFRNEN 372
QY 365 GILKXWISRPDVPYLETFAEDAAGEIAAELOGTDFDIFIGNYSDGNVVASLLSKMGVTO 424
Db 373 GILKXWISRPDVPYLETFAEDAAGEIAAELOGTDFDIFIGNYSDGNVVASLLSKMGVTO 432
QY 425 CNIAHALKTKYDPSDIYWKRFEDKXHFSCQSADLAMNHADFIITSTYQEIAGTKNTV 484

Db 433 CNIAHALKTKYDPSDIYWKRFEDKXHFSCQSADLAMNHADFIITSTYQEIAGTKNTV 492
QY 485 QYESHATFTLGLYRVVHGIDVDPKFNIVSPCADMSIYEPHTEK-AKRLTSLHSGTEN 543
Db 493 QYESHAKFTFPGGLYRVVHGIDVDPKFNIVSPCADMAIYFPFSEKOVCTLSLHRLIEQ 552
QY 544 LIYDPEQNDHEIGHLDLDRSKPIILFSMARLDRVKNITGLIVEAFKAKLRELVLNVVAGY 603
Db 553 LIFKPEQNEEHIGVLDLDTSPILFISMARLDRVKNITGLIVECYGKNAKRELANLVVAGY 612
QY 604 NDVVKSKDREELIABIEIKWHELIKTHNLFQGPRIWISAQTNBARNGELRYIADTHGAFVQP 663
Db 613 NDVVKSKDREELIABIEIKWHELIKTHNLFQGPRIWISAQTNBARNGELRYIADTHGAFVQP 672
QY 664 ALYEAFLGLTVVAMTCGLPTFATLHSGPAETIEHGVSGFHDVHPPEQAVNLMAFPDRC 723
Db 673 AFYEAFLGLTVVAMTCGLPTFATLHSGPAETIEHGVSGFHDVHPPEQAVNLMAFPDRC 731
QY 724 QODPDHWNTSGAGLQRIYKTYWIKYISERLMTLAGVYGFYKYSKLERLETRRYLEMFY 783
Db 732 REDNYWTKISAGSLLAKERYTWQKYSERLMTLAGVYGFYKYSKLERLETRRYLEMFY 791
QY 784 ILKPRELAKTVPLAIDQ 800
Db 792 ILKPRELANSVPLATDE 808
RESULT 10
Q92PCS PRELIMINARY; PRT; 811 AA.
AC Q92PCS;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13).
GN SS2.
OS Craterostigma plantagineum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; incertae sedis; Toreniaeae; Craterostigma.
OX NCBI_TaxID=4153;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=99396657; PubMed=10467027;
RA Kleines M., Elster R.C., Rodrigo M.J., Blervacq A.S., Salami F.,
RA Barrels D.;
RT "Isolation and expression analysis of two stress-responsive sucrose-
synthase genes from the resurrection plant Craterostigma plantagineum
(Hochst.)";
RL Planta 209:13-24 (1999).
DR EMBL; AT132000; CAB38022.1; -.
DR GO; GO:0016157; F:sucrose synthase activity; IEA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl. . .; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0005985; P:sucrose metabolism; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR InterPro; IPR00368; Sucrose synth.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00862; Sucrose synth_1; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 811 AA; 92523 MW; CF9C808F2BA80720 CRC64;
Query Match 77.4%; Score 3263; DB 10; Length 811;
Best Local Similarity 76.1%; Pred. No. 2.4e-232;
Matches 605; Conservative 93; Mismatches 95; Indels 2; Gaps 1;
QY 7 DRVEDTLAHNRNELVALLSKYVKNKGLIQPHHLDALDFV--QSGGRALAGPFLDVL 64
Db 14 ERVEDTLAHNRNELVALLSKYVKNKGLIQPHHLDALDFV--QSGGRALAGPFLDVL 73
QY 65 RSAQEAIVLPFVAIVAPRPGWVEYVRVNVHLSVEQLTVSEYLRPKBELVDGQNDPY 124
Db 74 RSAQEAIVLPFVAIVAPRPGWVEYVRVNVHLSVEQLTVSEYLRPKBELVDGQNDPY 133

RESULT 12

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Q9SBL8      PRELIMINARY;      PRT;      806 AA.
ID          AC
AC          Q9SBL8;
DT          01-MAY-2000 (TrEMBLrel. 13, Created)
DT          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT          01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE          WSUS.
GN          Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OS          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC          eurosid2; Cucurbitales; Cucurbitaceae; Citrullus.
OX          NCBI_TaxID=3654;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Kim J., Kang H., Jun S., Lee J., An G.;
RT          "Watermelon mRNA for GA3-regulated in developing seeds, complete cds.
RT          (Cloning of three gibberellin-regulated cDNAs from watermelon during
RT          early seed development: down-regulated one cDNA and up-regulated two
RT          cDNAs).";
RL          Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AB018561; BAA89232.1; -.
DR          GO; GO:0009058; P:biosynthesis; IEA.
DR          GO; GO:0005985; P:sucrose metabolism; IEA.
DR          InterPro; IPR001296; Glyco_trans_1.
DR          InterPro; IPR000368; Sucrose synth.
DR          Pfam; PF00534; Glycos_transf_1; 1.
DR          Pfam; PF00862; Sucrose synth; 1.
SQ          SEQUENCE      806 AA; 92559 MW; 4FD8EACD6C140337 CRC64;

Query Match      71.1%; Score 2998.5; DB 10; Length 806;
Best Local Similarity 70.2%; Pred. No. 8.7e-213;
Matches 560; Conservative 111; Mismatches 126; Indels 1; Gaps 1;

QY      3 HASGDRVEDTLHAHRELVALLSKYVKNKGKILQPHHILDALDEWQSGGGRALAEGLD 62
DB      10 HSLURERUDELIIAQRNBEILGILSKIEAKGKILQHQHILAEFEALPENRKKLAGDFGE 69
QY      63 VLRSACBAIVLPPFVALAIVPRPGVWYVYRVNHELVSVEQLTVSEYLFKBEYDGGHND 122
DB      70 VLRTQESIVLPPFVALAIVPRPGVWYVYRVNHELVAVEELQVAEYLHLKEELVDGSSNG 129
QY      123 PYVLELDFEFPNVSVPNPNSSSGTNGVQFLNRHLSIMFNRDCLPDLFLRGHREKG 182
DB      130 NFVLELDFEFPNASFPRTLSKSTGNGVFEFLNRHLLAKLPHGKESMQPDLFLRVHCYKG 189
QY      183 HVMNLDRIQSLGRQLSVLTKAEHLSKLPADTPYSQFAYKFBQWGLEKMGDTAGHVLE 242
DB      190 KTMNLDRIQTLNFAQVHLKAEYLANLADETPYSEFANKFEHIGLERGNGNTAERVLE 249
QY      243 MIHLLDIIQAPDPTLEKFLGRIPMIFNVVSPHGVFGQANVLGPDTCGQIVYILDQ 302
DB      250 MIQLLLEAPDPCTEKFLGRIPMVFNVILSPHGVFAQDNVLGYPDTCGQVYVYILDQ 309
QY      303 VRALENEMVLKQGLDVSFKILIVTRLIPDAKGTSCNQLERISCTQHTYILRVPERN 362
DB      310 VRALEHEMLQRIKQGLDITPRILIIITRLPDVAGTTCQLEKVFYGFTEHSHILRVPERN 369
QY      363 ENGLIKWISFDWVPLETEFAEDAAGIAELQCTPDIIGNYSDGNLVSLLSYKNGI 422
DB      370 EKGIVRWKISFEDWVPLETTEFVQBELTKELQKPDLLIGNYSDGNLVSLLANLKV 429
QY      423 TQCNIAHALEKTKYPCSDIFWKNFDEKVFSCQFTADIIAMNADFIITSTYQEIAGSKN 482
DB      430 TQCTIAHALEKTKYPCSDIYKRDYKVFSSQFTADLIAMNHTDFTITSTFQEIAGSKD 489
QY      483 TVGQVESHATLPLGLTRVWGHIDVDFPKFNVISFGADMSYFFHTEKAKLTSLGSGIE 542
DB      490 TVGQVESHATLPLGLTRVWGHIDVDFPKFNVISFGADMSYFFHTEKAKLTSFHPHIE 549
QY      543 NLIYDPEQNDGHIHLDDRSKPIFLSMARLDVRKNITGLVEYFAKCAKMLRELNVLVVAG 602

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550 ELLYSEVENEELCVLXDRSKPIIFTMARLDVRKNITGLVEYGNKKNKRLRELNVLVVAG 609
603 YNDVNSKDRBETAEIEEMHELKTHNLFCQFRMISACTPARNGELYRYIADTHGAFVQ 662
610 -DRRKESKDNEEKAEMKMYILIKTYNLNGQFRMISQOMNRVNGEVYRCIADTKGAFVQ 668
663 PALYAEAGLTWVEMTCTCLPTFATLHGGPABIIIEHGVSGPHIDPYHPQAVNLMADEFDR 722
669 PAVYAEAGLTWVEMTCTCLPTFATCNGGPABIIIDGSGFHIDPYRGDRAAEILVDFEK 728
723 CKQDPDHWNVISGAGLQRIYKTYTWKIVYSERIMTLAGYGVKVKVSKLERLETRYLEMP 782
729 SKEDPSHWDKISQAGLQRIYKTYWQIYSRLLTLTGWYGFWMKVNSNLDRESRYLEMP 788
783 YILKFERELAKTVPLAIDQ 800
789 YALKYRKLADSVPOAVDE 806

RESULT 13
Q8WIM4      PRELIMINARY;      PRT;      816 AA.
ID          AC
AC          Q8WIM4;
DT          01-MAR-2002 (TrEMBLrel. 20, Created)
DT          01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT          01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE          Sucrose synthase 2.
OS          Bambusa oldhamii (Giant timber bamboo).
OC          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC          Bambusoideae; Bambuseae; Bambusa.
OX          NCBI_TaxID=58923;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Lin C.-H., Wang A.-Y.;
RT          "Sucrose synthase in green bamboo Bambusa oldhamii.";
RT          Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AF412037; AAL50570.1; -.
DR          GO; GO:0009058; P:biosynthesis; IEA.
DR          GO; GO:0005985; P:sucrose metabolism; IEA.
DR          InterPro; IPR001296; Glyco_trans_1.
DR          InterPro; IPR000368; Sucrose synth.
DR          Pfam; PF00534; Glycos_transf_1; 1.
DR          Pfam; PF00862; Sucrose synth; 1.
SQ          SEQUENCE      816 AA; 92981 MW; EF4067896E51020D CRC64;

Query Match      70.9%; Score 2991; DB 10; Length 816;
Best Local Similarity 69.8%; Pred. No. 3.2e-212;
Matches 559; Conservative 108; Mismatches 126; Indels 8; Gaps 3;

QY      3 HASGDRVEDTLHAHRELVALLSKYVKNKGKILQPHHIL----DALDEWQSGGGRALAE 58
DB      14 HSVREIRGDSLSAHPNELVAVFTRLVNLGKGLQPHQIIAEYNNNAIPEARD---KLKDG 70
QY      59 PFLDVLRSACBAIVLPPFVALAIVPRPGVWYVYRVNHELVSVEQLTVSEYLFKBEYDVG 118
DB      71 AFEVPLRAQCAIVLPPFVALAIVPRPGVWYVYRVNHELVAVEELRVPEYLQFKSQLVEG 130
QY      119 QHNDPYVLELDFEFPNVSVPNPNSSSGTNGVQFLNRHLSIMFNRDCLPDLPLRGH 178
DB      131 STNNFVLELDFEFPNASFPRTLSKSTGNGVQFLNRHLSLKLFDKESMYPLNLELRAH 190
QY      179 RHKGHVWMLNDRIQSLGRQLSVLTKAEHLSKLPADTPYSQFAYKFBQWGLEKMGDGTAG 238
DB      191 NYKGMTWMLNDRIQSLGRQLSVLTKAEHLSKLPADTPYSQFAYKFBQWGLEKMGDGTAG 250
QY      239 HVLEMIHLLDIIQAPDPTLEKFLGRIPMIFNVVSPHGVFGQANVLGPDTCGQIVY 298
DB      251 RAQETIHLLEAPDPCTEKFLGRIPMVFNVILSPHGVFAQDNVLGYPDTCGQVYVY 310
QY      299 ILDOVRALENEMVLKQGLDVSFKILIVTRLIPDAKGTSCNQLERISCTQHTYILRV 358
DB      311 ILDOVRALENEMVLKQGLDVSFKILIVTRLIPDAKGTSCNQLERISCTQHTYILRV 370

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QY	359	PPRNGILKKWISRFDDVWPYLETFAEDAAGEIAAEALQGTDFPIIGNYSDGNLVASLSY	418
DB	371	PPRTENGIVRWISRFEEWPYLEITDDVAHEIAGELQANPDIIIGNYSDGNLVACILAH	430
QY	419	KMGICQCNIAHALEKTKYPPDSIDFWNFDEKXHFSCQFTADIANNADFIITSTYOBIA	478
DB	431	KMGVTHCTIAHALEKTKYPSNLDYWKFEEDVHFSCQFTDIIAMNHADFIITSTYOBIA	490
QY	479	GSKNTVGVESHATTLPLGLRVVHGIDVDFPKFNVSPGADMSIYFFPHTEKAKLTSLH	538
DB	491	GNKDTVGQTESHATTLPLGLRVVHGIDVDFPKFNVSPGADMSIYFFPHTEKAKLTSLH	550
QY	539	GSIELIYDPEQNDHEIGHLDKRPILFSPMARLDVRKNITGLVFAPAKCAKRLVNLV	598
DB	551	PIEIELLYSDVDNNEKFLVKDRNKPILFSPMARLDVRKNITGLVFAPAKCAKRLVNLV	610
QY	599	VWAGYNDVNSKDRREIABIEKMHILKTHNLFCQFRWISAOQNRNARNGELYRIADTHG	658
DB	611	VWCG-DHGNPSKDEQAEFKMFHIEQYINLGHIRWISAOQNRNARNGELYRIADTHG	669
QY	659	AFVQALYEAFLGTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHIDPYHPQAVNLMD	718
DB	670	AFVQALYEAFLGTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHIDPYHPQAVNLMD	729
QY	719	FFDRCKQDPDHWNISGAGLQRIYKTYKTIYSERLMTAGVYGFVKYVSKLERLTRY	778
DB	730	FFDRCKQDPDHWNISGAGLQRIYKTYKTIYSERLMTAGVYGFVKYVSKLERLTRY	789
QY	779	LEMYLKRELAKTVPILAID 799	
DB	790	LEMYLKRELAKTVPILAID 810	
RESULT 14			
ID	Q9SL52	PRELIMINARY; PRT; 805 AA.	
AC	Q9SL52		
DT	01-MAY-2000 (TREMBlrel. 13, Created)		
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)		
DE	Sucrose synthase.		
GN	CITSUS1-2.		
OS	Citrus unshiu (Satsuma orange).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Sapindales; Rutaceae; Citrus.		
OX	NCBI_TaxID=55188;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Miyagawa-wase;		
RA	Komatsu A.;		
RT	"Cloning of sucrose synthase (CITSUS1) gene from Citrus.";		
RT	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB29401; BAA89049.1; -		
DR	GO; GO:0005058; P:biosynthesis; IEA.		
DR	GO; GO:0005985; P:sucrose metabolism; IEA.		
DR	InterPro; IPR001296; Glyco trans 1.		
DR	InterPro; IPR000368; Sucrose synth.		
DR	Pfam; PF00534; Glycosynth_1.		
DR	Pfam; PF00862; Sucrose synth_1.		
SO	SEQUENCE 805 AA; 92172 MW; 2098FC1F524C266E CRC64;		
Query Match			
Best Local Similarity 69.6%; Pred. NO. 9.4e-212;			
Matches 555; Conservative 115; Mismatches 126; Indels 1; Gaps 1;			
QY	3	HASGRVEDTLAHNELVALLSKYVNGKGIQPHHILDALDEVGSGGRALAGPPLD	62
DB	10	HSLRRLDZTLASRNETALLSRIEKGKGLQNHQIABFESISERNRKHLETFGEAG	69
QY	63	VLRSAQEAIVLPPFVAJAVRPPGVWVYRVNVHLSVEQLTVSVLYLFKEELVDGQND	122
DB	123	PYVLELDEPFPNVSPRPNRSSIGNGVQFLNRHLSSIFNRNPDCLLELDLFLGRHNG	182
DB	130	NFVLELDEPFPNASPPRPTLSKISIGNGVQFLNRHLSSIFNRNPDCLLELDLFLGRHNG	189
QY	183	HWMLENDRIQSLGRISQSVLTAEHLSKLPADTPYSQPAYKFCBWLGEKMGDGTAGHVL	242
DB	190	KMMLENDRIQSLGRISQSVLTAEHLSKLPADTPYSQPAYKFCBWLGEKMGDGTAGHVL	249
QY	243	MTHLLDIIQAPDPSTLEKFLGRIPMIRNVVSVSHGYPQANVLGLDPTGGQIVVILQ	302
DB	250	MIQLLLDLEADPCTLETFLGRIPMIRNVVSVSHGYPQANVLGLDPTGGQIVVILQ	309
QY	303	VRLAENEMVRLKKGGLDVPKILAVRLIPDAKGTSCNQLERISGTOHTYILRVPERN	362
DB	310	VRLAENEMVRLKKGGLDVPKILAVRLIPDAKGTSCNQLERISGTOHTYILRVPERN	369
QY	363	ENGILKKWISRPDPWVPLETFAEDAAGEIAAEALQGTDFPIIGNYSDGNLVASLSY	422
DB	370	EKGVVKWISRPDPWVPLETFAEDAAGEIAAEALQGTDFPIIGNYSDGNLVASLSY	429
QY	423	TQNTAHLEKTKYPPDSIDFWNFDEKXHFSCQFTADIANNADFIITSTYOBIA	482
DB	430	TQNTAHLEKTKYPPDSIDFWNFDEKXHFSCQFTADIANNADFIITSTYOBIA	489
QY	483	TVGQYESHATTLPLGLRVVHGIDVDFPKFNVSPGADMSIYFFPHTEKAKLTSLH	542
DB	490	TVGQYESHATTLPLGLRVVHGIDVDFPKFNVSPGADMSIYFFPHTEKAKLTSLH	549
QY	543	NLIYDPEQNDHEIGHLDKRPILFSPMARLDVRKNITGLVFAPAKCAKRLVNLV	602
DB	550	ELLYSDVENKEHLKVLKDRNKPILFSPMARLDVRKNITGLVFAPAKCAKRLVNLV	609
QY	603	YNDVNSKDRREIABIEKMHILKTHNLFCQFRWISAOQNRNARNGELYRIADTHG	662
DB	610	-DRRKESKOLEQAEMKMYSLIDQYKINGQFRWISSQMRNVRNGELYRICITKGA	668
QY	663	PALYEAFLGTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHIDPYHPQAVNLMD	722
DB	669	PALYEAFLGTVVEAMTCGLPTFATLHGGPAEIIHGVSGFHIDPYHPQAVNLMD	728
QY	723	CKQDPDHWNISGAGLQRIYKTYKTIYSERLMTAGVYGFVKYVSKLERLTRY	782
DB	729	CKADPSYNDKISLGLAKRIEKKYKTIYSERLMTAGVYGFVKYVSKLERLTRY	789
QY	783	YILKRELAKTVPILAID 799	
DB	789	YALKYKLAESVPLAVE 805	
RESULT 15			
ID	Q8W1W3	PRELIMINARY; PRT; 808 AA.	
AC	Q8W1W3		
DT	01-MAR-2002 (TREMBlrel. 20, Created)		
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)		
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)		
DE	Sucrose synthase 1.		
OS	Bambusa oldhamii (Giant timber bamboo).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Bambusoideae; Bambuseae; Bambusa.		
OX	NCBI_TaxID=58923;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lin C.-H., Wang A.-Y.;		
RT	"Sucrose synthase in green bamboo Bambusa oldhamii.";		
RT	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF412038; AAL50571.1; -		
DR	GO; GO:0005058; P:biosynthesis; IEA.		
DR	GO; GO:0005985; P:sucrose metabolism; IEA.		
DR	InterPro; IPR001296; Glyco trans 1.		

[illegible]

Search completed: May 24, 2004, 11:25:19
Job time : 44.8218 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 17.424 Seconds
(without alignments)
4427.559 Million cell updates/sec

Title: US-10-080-114a-2
Perfect score: 4217
Sequence: 1 STHASGRVEDTLHAHREL.....YILKRELAKTVPLAIDQPQ 802

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	3456	82.0	809	probable sucrose s
2	3397.5	80.6	809	probable sucrose s
3	3366	79.8	808	sucrose synthase
4	3302	78.3	822	sucrose synthase
5	3045	72.2	804	sucrose synthase
6	2993.5	71.0	802	sucrose synthase
7	2990.5	70.9	808	sucrose synthase
8	2965	70.3	816	sucrose synthase
9	2944.5	69.8	805	sucrose synthase
10	2944.5	69.8	806	sucrose synthase
11	2922	69.3	816	sucrose synthase
12	2910.5	69.0	808	sucrose synthase
13	2904.5	68.9	808	sucrose synthase
14	2899	68.7	807	sucrose synthase
15	2861.5	67.9	801	sucrose synthase
16	2340.5	55.5	942	probable sucrose s
17	2259.5	53.6	586	sucrose synthase
18	1833	43.5	906	sucrose synthase
19	1506	35.7	805	sucrose synthase
20	843.5	20.0	235	sucrose synthase
21	778.5	18.5	212	sucrose synthase
22	739	17.5	204	sucrose synthase
23	681.5	16.2	179	sucrose synthase
24	587.5	13.9	218	sucrose synthase
25	515	12.2	127	sucrose synthase
26	467.5	11.1	720	hypothetical prote
27	466.5	11.1	1083	sucrose-phosphate
28	450	10.7	1056	sucrose-phosphate
29	445	10.6	1059	sucrose-phosphate

30	444	10.5	1068	1	J01329	sucrose-phosphate
31	441.5	10.5	1045	2	S55253	sucrose-phosphate
32	436.5	10.4	1053	2	S34172	sucrose-phosphate
33	433	10.3	1047	2	T51800	sucrose-phosphate
34	425	10.1	1054	2	T09833	sucrose-phosphate
35	414	9.8	1057	2	S72648	sucrose-phosphate
36	408.5	9.7	1081	2	T09837	sucrose-phosphate
37	401.5	9.5	1084	2	T04103	hypothetical prote
38	399	9.5	1064	2	R86182	sucrose-phosphate
39	351	8.3	1049	2	JC4783	sucrose synthase
40	325	7.7	100	2	T09856	glycosyltransferas
41	285	6.8	454	2	AG2657	hypothetical prote
42	285	6.8	454	2	D97439	sucrose-phosphate
43	248	5.9	341	2	S72649	hypothetical prote
44	226.5	5.4	923	2	G83826	sucrose-phosphate
45	221	5.2	348	2	S72650	sucrose-phosphate

ALIGNMENTS

RESULT 1

B85029
probable sucrose synthetase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: B85029
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: B85029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-809 <STO>
A:Cross-references: GB:NC_001268; NID:57268988; PIDN:CAH80721.1; GSPDB:GM00140
A:Gene: AT4G02280
A:Map position: 4
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

Query Match		82.0%; Score 3456; DB 2; Length 809;
Best Local Similarity		79.9%; Pred. No. 3 8e-223;
Matches		635; Conservative 89; Mismatches 69; Indels 2; Gaps 1;
QY	7	DRVEDTLHAHRELVALLSKYVNGKGILOPHILDALDEVQSG--GRALAEGPFLDVL 64
DB	14	DRVQDTLSAHRNELVALLSRYVDQKGILOPHNLIDELSEVICDDTKKSLSDGPFGEIL 73
QY	55	RSQAQAIIVLPFVAIVRPRGVWYVNVVHLSVQLTVSEYLFREKELVGGQNDPY 124
DB	74	KSAMEAIVVPPFVALAVRPRGVWYVNVVHLSVQLTVSEYLFREKELVGGQNDPY 133
QY	125	VLEDFEFPNVSPRPNRSSISGNGVQFLNRHLSSIMERNRDLCEPLDLFLGRHKGHV 194
DB	134	CLELDFEFPNVSPRPNRSSISGNGVQFLNRHLSSIMERNRDLCEPLDLFLGRHKGHV 193
QY	185	MLMDRIQSLGRQLSVLTAEHLKSLPADTYPQYKQFQWGLEKGGDGTAGHLEMI 244
DB	194	LMMDRIQSLGRQLSVLTAEHLKSLPADTYPQYKQFQWGLEKGGDGTAGHLEMI 253
QY	245	HLLELIIQAPDSTLEKLGRIPIVNVVSPHGVGOANVLGLPDTGQIVYILDQVR 304
DB	254	HLLELIIQAPDSTLEKLGRIPIVNVVSPHGVGOANVLGLPDTGQIVYILDQVR 313
QY	305	ALENEMWLKKGDLVSPKILIVTRLPDAKGTSCNQLERISGTQHTYILVRPFRNEN 364
DB	314	ALETEMWLKKGDLVSPKILIVTRLPDAKGTSCNQLERISGTQHTYILVRPFRNEN 373
QY	365	GILKRWISFDWPPYLETFAEDAAGSIAAELOCTPDIIGNYSDGNLVASLSYKNGITQ 424
DB	374	GILKRWISFDWPPYLETFAEDAAGSIAAELOCTPDIIGNYSDGNLVASLSYKNGITQ 433

QY 425 CNIAHALEKTYKPPDSIDIFWKNFDEKHFSCQFTADLIAMNADFIITSTYQEIAGSKNTV 484
 DB 434 CTIAHALEKTYKPPDSIDIFWKNFDEKHFSCQFTADLIAMNADFIITSTYQEIAGSKNTV 493
 QY 485 GQYESTHTAFTLPGLRVVGHDVDPKNIYSPGADMSIYPPHTBEKAKRLTSLHGSIEHL 544
 DB 494 GQYESTHTAFTLPGLRVVGHDVDPKNIYSPGADMSIYPPHTBEKAKRLTSLHGSIEHL 553
 QY 545 IYDPQNDHEHGHLDORSKPILFMSMARLDVRVXITGLVEAFKAKAKRELNLVNVVAGYN 604
 DB 554 LYSPPQTDHVGTLSDRSKPIFLFMSMARLDVRVXITGLVEAFKAKAKRELNLVNVVAGYN 613
 QY 605 DVNKSQRREIABIEKQHELIKTHNLFGQFRMISAGTRARNGELRYIADTHGAFVQPA 664
 DB 614 DVNKSQRREIABIEKQHELIKTHNLFGQFRMISAGTRARNGELRYIADTHGAFVQPA 673
 QY 665 LYAEAGLTVEAMTCGLPTFATLHGCPABIEIIEHVGSGPHIDPYHPEQAVNLMAFFDRCK 724
 DB 674 FYAEAGLTVEAMTCGLPTFATLHGCPABIEIIEHVGSGPHIDPYHPEQAVNLMAFFDRCK 733
 QY 725 COPDHVNVISAGLQRIYKTYKTIYSELMTLAGYVGFVKVSKLERLETRRYLEMFIY 784
 DB 734 EDENHWKXVSAGLQRIYKTYKTIYSELMTLAGYVGFVKVSKLERLETRRYLEMFIY 793
 QY 785 LKFERLAKTVPLAID 799
 DB 794 LKFERLAKTVPSTAD 808
 RESULT 2
 T06497
 probable sucrose synthase (EC 2.4.1.13) 2 - garden pea
 C:Species: Pisum sativum (garden pea)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2003
 C:Accession: T06497
 R:Buchner, P.
 submitted to the EMBL Data Library, October 1997
 A:Reference number: Z15720
 A:Accession: T06497
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-809 <BUC>
 A:Cross-references: EMBL:AJ001071; PIDN:CAA04512.1
 A:Experimental source: cultivar Frisson
 C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
 C:Keywords: glycosyltransferase; hexosyltransferase
 F:282-757/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
 Query Match 80.6%; Score 3397.5; DB 2; Length 809;
 Best Local Similarity 78.9%; Pred. No. 3.1e-219; Indels 9; Gaps 2;
 Matches 636; Conservative 80; Mismatches 81
 QY 1 STE-----ASGDRVEDTLHAHRELVALLSKYVNGKGILOPHHILDALDEVQSGGR 53
 DB 2 STHPKTRVPSIRDVQDTLSAHRNELISLSRYVAQKGILQPHNLIDELNDILGEDHA 61
 QY 54 A--LAEGPFLDVLRSQAELVLPFAIAVRPPGWWEYVRVNVHLSVEQLTVSEYLR 111
 DB 62 TLIDKNGPFQIINSAQAELVLPFAIAVRPPGWWEYVRVNVFELSVEQLSVSEYLSF 121
 QY 112 KEELVQGNQNDPVVLELDFEPNVSVPRNRSSIGNGVQFLNRHLSSIMFRNRDCLPL 171
 DB 122 KEELVEKSNNDNIIEULCEBFFNAPFRPRTRSSIGNGVQFLNRHLSSIMFRNRDCLPL 181
 QY 172 LDFLRGHRHKGHWMLMDRIQSLGRLOSILTKABEHLISKLPADTPYSQAYKQEWGLEK 231
 DB 182 LDFLRVHTYKGHMLMDRIQSLKQSLQALVKAEDHLSKLPADTPYSEFEYELQGTGER 241
 QY 232 GWGSDTAGHVLKMLHLLDITQADPSTLEKFLGRIPMFVNVVSVSPGYGQANVLGLPD 291
 DB 242 GWGSDTAARVLEWMHLLDILQADPSTLETFLGRVPVNVFVNVVILSPHGFQANVLGLPD 301
 QY 292 TGSQIVVILQVRALENEMVRLKKGQGLDVSEKILLIVTRLIPDAKGTSCQRLERISGTQ 351

DB 302 TGGQVVVILQVRALESMLVRIKKQGLDFTPRILLIVTRLIPDAKGTTCQRLERSVGTG 361
 QY 352 HTYILVRFRBENGILKWIISRFDVWPLYETFAEBAAGIAEALOGCTPDIIGNYSDGNL 411
 DB 362 YTHILVRFRBENGILKWIISRFDVWPLYETFAEBAAGIAEALOGCTPDIIGNYSDGNL 421
 QY 412 VASLLSYKMGITQCNIAHALEKTYKPPDSIDIFWKNFDEKHFSCQFTADLIAMNADFIIT 471
 DB 422 VASLLAYKMGITQCNIAHALEKTYKPPDSIDIFWKNFDEKHFSCQFTADLIAMNADFIIT 481
 QY 472 STYQBIAGSKNTVGOYESTHTAFTLPGLRVVGHDVDPKNIYSPGADMSIYPPHTBEKA 531
 DB 482 STYQBIAGSKNTVGOYESTHTAFTLPGLRVVGHDVDPKNIYSPGADMSIYPPHTBEKA 541
 QY 532 KRLTSHGSIEHLIYDPQNDHEHGHLDORSKPILFMSMARLDVRVXITGLVEAFKAKAK 591
 DB 542 KRLTSHGSIEHLIYDPQNDHEHGHLDORSKPILFMSMARLDVRVXITGLVEAFKAKAK 601
 QY 592 RELVNLVVAGYNDVNVKSKDREIABIEKQHELIKTHNLFGQFRMISAGTRARNGELRY 651
 DB 602 RELVNLVVAGYNDVNVKSKDREIABIEKQHELIKTHNLFGQFRMISAGTRARNGELRY 661
 QY 652 YIADTEGAFVQPALYEAFTLVEAMTCGLPTFATLHGCPABIEIIEHVGSGPHIDPYHPEQ 711
 DB 662 YIADTEGAFVQPALYEAFTLVEAMTCGLPTFATLHGCPABIEIIEHVGSGPHIDPYHPEQ 721
 QY 712 AVNLMAFFDRCKQDPPDHVNVISAGLQRIYKTYKTIYSELMTLAGYVGFVKVSKLER 771
 DB 722 ASELAIVDFORCKEDPNHWKXVSAGLQRIYKTYKTIYSELMTLAGYVGFVKVSKLER 781
 QY 772 RLETRRYLEMFIYKPRELAKTVPLA 797
 DB 782 RRETRRYLEMFIYKPRELANSVPIA 807
 RESULT 3
 T01420
 sucrose synthase (EC 2.4.1.13) T2H3.8 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999
 C:Accession: T01420
 R:Kalicki, J.; Gibson, A.
 submitted to the EMBL Data Library, August 1998
 A:Description: The sequence of A. thaliana T2H3.
 A:Reference number: Z14324
 A:Accession: T01420
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-808 <KAL>
 A:Cross-references: EMBL:AF075597; NID:G3298610; PIDN:AAC28175.1; PID:G3377802
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 4
 A:Introns: 33/2; 77/3; 192/3; 304/3; 327/2; 421/3; 477/2; 552/2; 659/3; 741/2
 A:Note: T2H3.8
 C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
 C:Keywords: glycosyltransferase; hexosyltransferase
 F;281-744/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
 Query Match 79.8%; Score 3366; DB 2; Length 808;
 Best Local Similarity 78.9%; Pred. No. 4e-217;
 Matches 620; Conservative 88; Mismatches 64; Indels 14; Gaps 2;
 QY 7 DRYEDTLHAHRELVALLSKYVNGKGILOPHHILDALDEVQSG--GRALAEQPPLOVL 64
 DB 14 DRYQDTLSAHRNELVALLSRYVDQKGILQPHNLIDELSVIGDDETKSLSGDPFEIL 73
 QY 65 RSQAELVLPFAIAVRPPGWWEYVRVNVHLSVEQLTVSEYLRPFKEBELVDQSHNDPY 124
 DB 74 KSQAELVLPFAIAVRPPGWWEYVRVNVFELSVEQLTVSEYLRPFKEBELVDGPNDDPF 133
 QY 125 VLDELDFEPNVSVPRNRSSIGNGVQFLNRHLSSIMFRNRDCLPLDLFLGRHHRKHV 184

Db 134 CLELDPEFNANVPRPSSSSGNGVQFARHLSSVFNKNCOCLEPLDLFLRVHXYKQHP 193
QY 185 MMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEWGLEKSGWGTAGHVLMI 244
Db 134 LMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEWGLEKSGWGTAGHVLMI 253
QY 245 HLLDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYILDQVR 304
Db 254 HLLSDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYILDQVR 313
QY 305 ALENEMVLRLKQGLDVSPKLLIIVTRILPDAGTSCNORLERISCTOHTYILRVPEREN 364
Db 314 ALETEMILLRIKROG-----LIPDAKGTTCNORLERSVTEGTHILRVPFSEK 361
QY 365 GILKWTISRFDVWPYLETFABDAAGEAAELQGTDFIIGNYSDGNLVSLLSYKMGITQ 424
Db 362 GILKWTISRFDVWPYLETFABDAAGEAAELQGTDFIIGNYSDGNLVSLLSYKMGITQ 421
QY 425 CNIAHALEKTKYPSDIFWKNFDEKYPHSCOPTADIAMNNADFIITSTYQEIAGSKNTV 484
Db 422 CTIAHALEKTKYPSDIFWKNFDEKYPHSCOPTADIAMNNADFIITSTYQEIAGSKNTV 481
QY 485 GOYESHAFITLPGLYRVVHGIDVDPKFNIVSPGADWSIYEPHTEKAKRLTSLHGSINL 544
Db 482 GOYESHGAFITLPGLYRVVHGIDVDPKFNIVSPGADWTIYPPYSEETRLTALHGSIEEM 541
QY 545 IYDPEQNDHEIGHLDSDRSKPIILFMSMARLDVRKNITGLVEAFKAKAKRELNLVVVAGYN 604
Db 542 LYSPODQDEHVGTLSDRSKPIILFMSMARLDVRKNITGLVEAFKAKAKRELNLVVVAGYN 601
QY 605 DVNKSXDREIEAEIKKHHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 664
Db 602 DVNKSXDREIEAEIKKHHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 661
QY 665 LYFAFGITVVEAMTCGLPTFATLHGGPAEIIHGVSGPHIDYHPEQAVNLMAFFEDRCK 724
Db 662 FYFAFGITVVEAMTCGLPTFATLHGGPAEIIHGVSGPHIDYHPEQAVNLMAFFEDRCK 721
QY 725 QDPDHWNIISGAGLQRIYKTYKTIYSERLMTLAGVYGFYKVKSLERLERRYLEMFI 784
Db 722 EDPNHKKVSDAGLQRIYKTYKTIYSERLMTLAGVYGFYKVKSLERLERRYLEMFI 781
QY 785 LKFRDL 790
Db 782 LKFRDL 787

RESULT 4

S71493
sucrose synthase (EC 2.4.1.13) - beet
C:Species: Beta vulgaris (beet)
C:Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
C:Accession: S71493; S71494
R:Hesse, H.; Willmitzer, L.
Plant Mol. Biol. 30, 863-872, 1996
A:Title: Expression analysis of a sucrose synthase gene from sugar beet (Beta vulgaris L.)
A:Reference number: S71493; MUID:96270366; PMID:8633746
A:Accession: S71493
A:Molecule type: mRNA
A:Residues: 1-822 <HES>
A:Cross-references: EMBL:X81974
R:Hesse, H.; Willmitzer, L.
submitted to the EMBL Data Library, September 1994
A:Description: Molecular cloning of a mitochondrial isoform of Cysteine Synthase from Ar
A:Reference number: S71494
A:Accession: S71494
A:Molecule type: mRNA
A:Residues: 'AG', 59-822 <HEW>
A:Cross-references: EMBL:X81974; NID:g1488569; PIDN:CAA57493.2; PID:g1488570
A:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:280-755/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

RESULT 5

YUMU

sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999
C:Accession: S19125
R:Chopra, S.; Del-Valero, J.; Dolferus, R.; Jacobs, M.
Plant Mol. Biol. 18, 131-134, 1992
A:Title: Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization.
A:Reference number: S19125; MUID:92119221; PMID:1531031
A:Accession: S19125

Query Match 78.3%; Score 3302; DB 2; Length 822;
Best Local Similarity 78.3%; Pred. No. 7.8e-213;
Matches 624; Conservative 80; Mismatches 89; Indels 4; Gaps 3;
QY 7 DRVEDTTLHAHRELVALLSKYVNGKGLIQPHHILDALDEVQ--SGGRALAAEGPFLDVL 64
Db 13 ERVEDTTLVHRELVALLSKYVNGKGLIQPHHILDGLESVIGEDKQILSDGPFSEVL 72
QY 65 RSAQEAIVLPFFVAIVAPRPGVMEYVNVVHLSVQSLTVSEYLRFKBELVDGQNDY 124
Db 73 RSAQEAIVLPFFVAIVAPRPGVMEYVNVVHLSVQSLTVSEYLRFKBELVDGKADHY 132
QY 125 VLELDFEENVSVPRESSSGNGVQFNHLSLIMERNRDCLEPLDLFLRHGHKGV 184
Db 133 VLELDFEENVSVPRTSSSGNGVQFNHLSLSSMFCNCKCLEPLDLFLRVHKGWV 192
QY 185 MMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKFOEWGLEKSGWGTAGHVLMI 244
Db 193 MMLNDRIQTIQRLQSAKSAEDYLIKLPADTPYSEFEVIOGMGFERGWDIAERVLEMM 252
QY 245 HLLDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYILDQVR 304
Db 253 HLLDIIQAPDPSTLEKFLGRIPMIENVVVSPHGYFGQANVLGLPDTGGQIVYILDQVR 312
QY 305 ALENEMVLRLKQGLDVSPKLLIIVTRILPDAGTSCNORLERISCTOHTYILRVPEREN 364
Db 313 SLEHMLQRIKKQGLDVTPLIIVSRLLIPDAKGTTCNORMEKVSGTEHASIILRVFRSEK 372
QY 365 GILKWTISRFDVWPYLETFABDAAGEIAAEELQGTDFIIGNYSDGNLVSLLSYKMGITQ 424
Db 373 GILKWTISRFDVWPYLETFABDAAGEIAAEELQGTDFIIGNYSDGNLVSLLSHRMGTQ 432
QY 425 CNIAHALEKTKYPSDIFWKNFDEKYPHSCOPTADIAMNNADFIITSTYQEIAGSKNTV 484
Db 433 CNIAHALEKTKYPSDIFWKNFDEKYPHSCOPTADIAMNNADFIITSTYQEIAGSKNTV 492
QY 485 GOYESHAFITLPGLYRVVHGIDVDPKFNIVSPGADWSIYEPHTEKAKRLTSLHGSIN 543
Db 493 GOYESHGAFITLPGLYRVVHGIDVDPKFNIVSPGADMAIYFFSEKDVTCILSLHRLIQ 552
QY 544 IYDPEQNDHEIGHLDSDRSKPIILFMSMARLDVRKNITGLVEAFKAKAKRELNLVVVAGY 603
Db 553 LLFPEQNEEHLGVLDITSKPIILFMSMARLDVRKNITGLVEAFKAKAKRELNLVVVAGY 612
QY 604 DVNKSXDREIEAEIKKHHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 663
Db 613 NDVKKSDREIEAEIKKHHLIKTNLFGQFNWISAGQTNRAENGELRYRIADTHGAFVOP 672
QY 664 ALYFAFGITVVEAMTCGLPTFATLHGGPAEIIHGVSGPHIDYHPEQAVNLMAFFEDRC 723
Db 673 AFYFAFGITVVEAMTCGLPTFATLHGGPAEIIHGVSGPHIDYHADQA-EKMTFFVVC 731
QY 724 QDPDHWNIISGAGLQRIYKTYKTIYSERLMTLAGVYGFYKVKSLERLERRYLEMFI 783
Db 732 REDPNYWKISAGGLRIKERTYKQYSEKLMILAGVYGFYKVKSLERLERRYLEMFI 791
QY 784 ILKFRDLAKTVPIADQ 800
Db 792 ILKFRDLANSVPLATDE 808

A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-804 <CHO>
A;Cross-references: EMBL:X60987; NID:g16525; PIDN:C2A43303.1; PID:g16526
C;Genetics: 72.28; Score 3045; DB 1; Length 804;
C;Introns: 31/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/2; 559/2; 666/2
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;276-750/Domain: sucrose-phosphate synthase homology <SSPS>

	Query Match	Best Local Similarity	Matches	571; Conservative	73.3%; Pred. No. 1.2e-195;	98; Xismatches	104; Indels	6; Gaps	4;
Qy	24	LSKVNKGKGLQPHHLLDA-LDEVQSGG-RALAEQFFLDVLRSQAQAIVLPPFVAIAV	81						
Db	29	LVRVVAHGKGLQSHQLIDFLKTVKVDGTLEDLNKSPFMKVL--QEAIVLPFFVALAI	85						
Qy	82	RPRGVWYVYVNVVHEIUSVQLTVSEVLRKEELVDGQNDPVLHLCPPFNVSVPRPN	141						
Db	86	RPRGVREYVYVNVVYELSDHLTVSEVLRKEELVNGHANGDYILLEHFPFNFATLPRPT	145						
Qy	142	RSSISNGVQFLAPHLSSIMFRNDCLEPLDLFRLGRHHRKHGMVMLNDRISQLRQSVL	201						
Db	146	RSSISNGVQLVNNHLLSSIMFRNKSEPELLEFRLTHKHGGRPMMLNDRINQTLPGAL	205						
Qy	202	TKABEHLKSLPADTPYSQFAYKFQEWLEKGGWGTAGVLEMIHLADLIQAPDPSTLEK	261						
Db	206	ARAEFLSKLPLATPYSEFPELQVGFERGWTQAKVSEMVHLLADILQAPDPVLET	265						
Qy	262	FLGRIPMFNVVVVSPHGYQGANVLGLPDTGGQIVVILDOVRALENMVLKKGGLDV	321						
Db	266	FLGRIPMVFNVILSRGYGAQANVLGLPDTGAQVYVILDOVRALENMILLRQKQGLEV	325						
Qy	322	SPKILVIRLIPDAKGTSCNORLERISGTOHTYILRVPFRNENGLKKTWSRFDVWYLE	381						
Db	326	IPKILVIRLIPDAKGTSCNORLERISGTOHTYILRVPFRNENGLKKTWSRFDVWYLE	385						
Qy	382	TFADAAAGEIAAELQGTPOFTIGNYSQNLVASLSYKMGITQCKIAHALEKTKYPDSI	441						
Db	386	TFADASNEISAEELQGVPLNLIIGNYSQNLVASLSLAKLGVIOCKIAHALEKTKYPDSI	445						
Qy	442	FWKPFDSKYPHSCOFTADLIAMNNADFIITSTYQEIAGSKNTVQYQESHFTLPGLYRV	501						
Db	446	YWRNHEDKYPHSSOFTADLIAMNNADFIITSTYQEIAGSKNNVQYQESHFTLPGLYRV	505						
Qy	502	VHGIDVDEKENIVSPGADMSIYPPHYTKAKRLTSLHGSIMLIYDPQONDEHIGHLDDR	561						
Db	506	VHGIDVDEKENIVSPGADMTIYPPYSDKERRILTAHIESIELLSFAEQNDHEVGLLSQ	565						
Qy	562	SKPILFSMARLDRVKNITGLVEAFKACKLRELVNVVAGYNDVNVKSKDREETAEIKM	621						
Db	566	SKPIIFSMAFLDRVKNLTGLVECAKNSKURELANLVITGVGYIDENOSRDREEMAEIQM	625						
Qy	622	HELLKTNLFCQPHISQAQWRAENGELRYIADTHGAFVQPALVEAGLTVVAMTCGL	681						
Db	626	HSLEQYDLHGEFFWAAQMNVRVNGELRYIADTKGVFVQPAFYEPGLTVVSMTCAL	685						
Qy	682	PTFATLHGGPABIIETHGSGPHIDPHYDHPQAVNLMADEFFDRCKQDPDHVNVISAGLQRI	741						
Db	686	PTFATCHGGPABIIETHGSGPHIDPHYDHPQAVAGSLA-LFETCTNPNHVWVISEGLKRI	744						
Qy	742	YEYTWKIYSRLMTLAGYGFMYKTVSKLERLETRRYILEMFIYLFKRELAKTVPLAIDQ	800						
Db	745	VERYTWKYSRLMTLAGYAFMKHVSKLRETRRYILEMFIYSLKFRDLANSIPLATDE	803						

RESULT 6
YUZMS
sucrose synthase (EC 2.4.1.13) - maize
C_Species: Zea mays (maize)
C_Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #ext_change 11-Jun-1999
C_Accession: S37184; S19085

R:Werr, M.; Frommer, W.B.; Maas, C.; Starlinger, P.
EMBO J. 4, 1373-1380, 1985
A:Title: Structure of the sucrose synthase gene on chromosome 9 of Zea mays L.
A:Reference number: S071184
A:Accession: S071184
A:Molecule type: DNA
A:Residues: 1-802 <WER>
A:Cross-references: EXBL:X02382; NID:g22487; PIDN:CAA36225.1; PID:g22488
A:Accession: S19085
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-802 <WER2>
A:Cross-references: EXBL:X02400; NID:g22485; PIDN:CAA36247.1; PID:g22485
C:Genetics:
A:Gene: sh
A:Map position: 9
A:Introns: 32/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/2; 559/2; 666/2
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
E:276-750/nominal: sucrose-phosphate synthase homology <SSPS>

Query Match	71.0%;	Score 2993.5;	DB 1;	Length 802;
Best local similarity	70.0%;	Pred. No. 3.3e-192;		
Matches 558;	Conservative 105;	Mismatches 131;	Indels 3;	Gaps 2;
QY	3	HASDRYEDTLLAHNELVALLSKYVKNKGILQPHILDALDEVOGSGRAALAEGLFD	62	
DB	9	HSLRERLCATFSSHPNELIALFSRYVHQKMLQRHQLLAEEFDALFDSDEKYA--FPED	66	
QY	63	VLRSAQEAIVLPPFVALAVRPPGVVYRVNVNHELVSQGLTWTSEYLRPKBELVDGQND	122	
DB	67	ILRAAQEAIVLPPWVALAIRPPGVWDYIRKVNSELAVELSVSEYLAFAKEQLVDGQSN	126	
QY	123	PYVLELDFEPENVSVPNPNRSSISGNGVQFINRHLSIMFNRNCLLEPLDPLFGRHRHG	182	
DB	127	NFVLELDFEPFNASFPNPSMKSISGNGVQFINRHLSKLPQDKKESYPLNLFLLKARHVF	186	
QY	183	HVMMLNRIQSLGRQSLVLTAKAEHLSKLPAITYSOFAYKFOEWGLEKMGMDTAGHVLE	242	
DB	187	TTMLNRIQSLRGQSLRKAEBYLLSVPODITYSEFNRPQELGLEKMGDTAKRVLD	246	
QY	243	MIHLLDIIQAPDPSTLEKFLGRIPMIFVNVVSPHGYFGQANVLGPDPTGGQIVYILDQ	302	
DB	247	TLHLLDLLLEAPDPANLEKFLGTIPWMFNVVILSPHGYFAQSNVLGYPD*GGQVYVILDQ	306	
QY	303	VRALENEMVLRKKQGLDVSFKPILIVRLTPDAKGTSCNQRLEKISGTHFTYILRVPERN	362	
DB	307	VRALENEMLLRKKQGLDITPKILIVLTRLLEPDAAGITTCGQLEKIVGTGHTTILRVPERN	366	
QY	363	ENGILKKWISRFOWPVLTEPAEDAAGHIAAELQTPDIFILGNYSQGNLVASLLSYKGI	422	
DB	367	ENGILKKWISRFOWPVLTEPDSVSSEIMKEMQAKPDLIIIGNYSDGNLVATLLAHKLVG	426	
QY	423	TQCNIAHALEKTKYPSDIPFKNFDEKYHFSCQPTADIIAMNADFIITSTYQHIAGSKN	482	
DB	427	TQCTIAHALEKTKYPSNDIYLDKDSQYHFSCQPTADLIAMNHTDFIITSTFQBIAGSKD	486	
QY	483	TVGQYESHTAFTLPGLYRVVHGIDVDPKFNIVSPGADMSIYFPFTEKAKELTSLHGSIE	542	
DB	487	TVGQYESHIAFTLPGLYRVVHGIDVDPKFNIVSPGADMSVYYPYTEDTKRLTAFHPDIE	546	
QY	543	NLIYDPEONDEHIGHLDRSKPILFMSMARLDVRKNIITGLVEAFAKAKRLRLNVLVVAG	602	
DB	547	ELIYSDVENSEHKFVLDKKKPIIFMSMARLDVRKNTGLVEMYGKARLRELANLIVVAG	606	
QY	603	YNDVNKSKDREIEAIEKOMEHLIKTHNLFGQFRWISAQTNPARNGELVRYIYADTHGAFVQ	662	
DB	607	-DHGKESKDREEQAEFKQWYSLIDYKLGKHIRWISAQNNRVNRNGELVRYICTDKGAFVQ	666	
QY	663	PALYEAFLTVVEAMTCGLPTFATLHGCPAELIIEHGVSGFPHIDPYPHQAVNLMADEFDR	722	
DB	666	PAFYEAFLGTWIESMTCSGLPTIATCHGCPAELIIVDGVSLGHIDPYSKADAILVNFDEK	726	


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Db      14  HSVREIRGSLSAHNELVAVFTRLVNKGMLQAHQIIAEYNNALSEADREKLDKGAPE 73
QY      62  DVLSAQBAIVLPPFAIAVPRPGVWEYVRNVNHELSSVEQLTVSEYLRPFKEELVDGQIN 121
Db      74  EVLSAQEGIVISPVVALAIRPRPGVWEYVRNVNSELAVELLTVPEYLOFKEQLVEEGTN 133
QY      122  DRYVLELDEPEPNVSPRENSSSTGNGVQFELNRHLSSTMERNRDCEPLDPLFLRHHRK 181
Db      134  NNFVLELDEPEPNABFPRESLSKSGNGVQFELNRHLSKFLFDKESMYFLNPLRAHNYK 193
QY      182  GHWMLNDRIOQLRGLQSVLTAKAEHLSKLPADTPYSQFAYKFOEMGLEKMGDGTAGHYL 241
Db      194  GWTMLNDRISLSALQALRAKAEHLSGLSADTPYSEFPHRFQELGLEKMGDCAKRSQ 253
QY      242  EMHLLDIIQAPDPSLTSEKFLGRIPMIINNVVVSHPGYFGQANVLGLDPTGGQIYVILD 301
Db      254  ETIHLLDLEAPDPSLTSEKFLGRIPMIINNVVVSHPGYFGQANVLGLDPTGGQVYVILD 313
QY      302  QVRALENEVLRLLKQGLDVSPLILVTRLIIPDAKGTSCNORLERISGTOHTVILRVPR 361
Db      314  QVRAMENMLLRKIQGLWITPKILIVTRLPDAGTTCQRLKVKLVGHEHTHLRVPR 373
QY      362  NENGILKMWISPDVWPYLETFAEDAAGETAABELQCTPDFIIGNYSDGNLVASLLSYXMG 421
Db      374  TENGIVRKWISPEVWPYLETFTDDVAHELAGELQAMPDLIIGNYSDGNLVACILAHMG 433
QY      422  ITQCNIAHALEKTKYFDSILFWKNFDEKHFSCQFADIIAMNADFIITSTYOEIAGSK 481
Db      434  VTHCTIAHALEKTKSPNSDLYWKKFEDHYKFSQCTTDLIAMNADFIITSTYOEIAGNK 493
QY      482  NTVGQYESHTAFTPLGLYRVVHGIDVDPKFNTPSPGADMSIYPPHTEKAKRLTSLHGI 541
Db      494  DTVGQYESHMAFTMPGLYRVVHGIDVDPKFNTPSPGADMSIYPPHTEKAKRLTSLHPEI 553
QY      542  ENLIYDPEQNDHEIGHLDSDSKPILFSMARLDVKNITGLVEAPAKCAKRLVNLVVA 601
Db      554  EELLYSEVDNNEHKFMLKDRNKPILFSMARLDVKNITGLVEAPAKCAKRLVNLVVA 613
QY      602  GYNDVNSKDRBEIAEIKHHELIKTHNLFGQFRWISQATNRARNGELYRYIADTHGAFV 661
Db      614  G-DHGNSPKDKEQAEFKCMFDLEQNLNGHIRMWISQATNRARNGELYRYIADTHGAFV 672
QY      662  OPALYEAFTLVVEAMTGLPTFATLGGPAEIIIEHGVSGFHDIPHEQAVNLMDFFD 721
Db      673  QPAFYEAFTLVVESMTCGLPTFATLGGPAEIIIEHGVSGFHDIPYQGDKASALLVEFFE 732
QY      722  RCKQDPDHWNISGAGLQRIYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRRYLEM 781
Db      733  KCQDPDHWNISGAGLQRIYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRRYLEM 792
QY      782  FYILKRELAKTVPLAID 799
Db      793  LYALKYRTMASTVPLAVE 810

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RESULT 9

YUPOS
sucrose synthase (EC 2.4.1.13) - potato
C:Species: Solanum tuberosum (potato)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C:Accession: A29615
R:Salanoubat, M.; Belliard, G.
Gene 60, 47-56, 1987
A:Title: Molecular cloning and sequencing of sucrose synthase cDNA from potato (Solanum tuberosum)
A:Reference number: A29615; MUID:88152501; PMID:2964386
A:Accession: A29615
A:Molecule type: mRNA
A:Residues: 1-805 <S>
A:Cross-references: GB:M18745; MID:g169571; PIDN:AAA33841.1; PID:g169572
A:Experimental source: var. Sirrema 2n=4x
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase

F:279-753/Domain: sucrose/sucrose-phosphate synthase homology <SSP>

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Query Match      69.8%; Score 2944.5; DB 1; Length 805;
Best Local Similarity 68.9%; Pred. No. 6.4e-189;
Matches 549; Conservative 115; Mismatches 132; Indels 1; Gaps 1;

QY      3  HASGDRVEDTLHAHRELVALLSKYVKNKGILQPHHILDALDEVOGSGRALARGPFLD 62
Db      10  HSLRERVDATLAHRNEILLFLSRBESHGKILKPHLEAFDAIRQDDCKKNEHAFEE 69
QY      63  VLRSQEAIVLPPFAIAVPRPGVWEYVRNVNHELSSVEQLTVSEYLRPFKEELVDGQIN 122
Db      70  LLKSTOEALVLPFWALAIRPGVWEYVRNVNHELSSVEQLTVSEYLRPFKEELVDGASNG 129
QY      123  PYVLELDFEPFNVSPRPNRSSISNGVQFELNRHLSSTMERNRDCEPLDPLFLRHHRK 182
Db      130  NFVLELDFEPFNTASFPKPLTKSINGVQFELNRHLSAKMFDKESMTPLLEPLRAHRYK 189
QY      183  HVMMLNDRIOSLGRJQSVLTAKAEHLSKLPADTPYSQFAYKFOEMGLEKMGDGTAGHYL 242
Db      190  KTMMLNDRIQNSNTLQNLVLRKABEYLIMLPPTPYFEHKEFQELGLEKMGDGTABRVLE 249
QY      243  MHLHLDIIQAPDPSLTSEKFLGRIPMIINNVVVSHPGYFGQANVLGLDPTGGQIYVILD 302
Db      250  MVMMLDLLEAPDPSLTSEKFLGRIPMIINNVVVSHPGYFGQANVLGLDPTGGQVYVILD 309
QY      303  VVALENEVLRLLKQGLDVSPLILVTRLIIPDAKGTSCNORLERISGTOHTVILRVPRN 362
Db      310  VPALERMLKRIKEQGLDIIIPRILIVTRLPDAGTTCQRIKVKYGAEHSHILRVPRFT 369
QY      363  ENGLKKNISRPDWPYLETFAEDAAGETAABELQCTPDFIIGNYSDGNLVASLLSYXMI 422
Db      370  EKVIVKMWISRPDWPYMETFIEDVAKEISAELOAKPDLIIGNYSDGNLVASLLAHKLV 429
QY      423  TQCNIAHALEKTKYFDSILFWKNFDEKHFSCQFADIIAMNADFIITSTYOEIAGSKN 482
Db      430  TQCTIAHALEKTKYFDSILFWKNFDEKHFSCQFADIIAMNADFIITSTYOEIAGSKD 489
QY      483  TVGQYESHTAFTPLGLYRVVHGIDVDPKFNTPSPGADMSIYPPHTEKAKRLTSLHSGIE 542
Db      490  TVGQYESHMAFTMPGLYRVVHGIDVDPKFNTPSPGADMSIYPPHTEKAKRLTSLHSGIE 549
QY      543  NLIYDPEQNDHEIGHLDSDSKPILFSMARLDVKNITGLVEAPAKCAKRLVNLVVA 602
Db      550  ELLYSVDNNEHKFMLKDRNKPILFSMARLDVKNITGLVEAPAKCAKRLVNLVVA 609
QY      603  YNDVNSKDRBEIAEIKHHELIKTHNLFGQFRWISQATNRARNGELYRYIADTHGAFV 662
Db      610  -DRKESKDLSEQAEKMKMVELIETHNLNGQFRWISQATNRARNGELYRYIADTHGAFV 668
QY      663  PALYEAFTLVVEAMTGLPTFATLGGPAEIIIEHGVSGFHDIPHEQAVNLMDFFDR 722
Db      669  PAFYEAFTLVVEAMTGLPTFATLGGPAEIIIEHGVSGFHDIPHEQAVNLMDFFDR 728
QY      723  CKQDPDHWNISGAGLQRIYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRRYLEM 782
Db      729  CKQDPDHWNISGAGLQRIYKTYKLYSERLMTLAGVYGFVKYVSKLERLETRRYLEM 788
QY      783  FYILKRELAKTVPLAID 799
Db      789  YALKYRTMASTVPLAVE 805

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RESULT 10

S31479
sucrose synthase (EC 2.4.1.13) - fava bean
C:Species: Vicia faba (fava bean)
C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: S31479
R:Heim, U.; Weber, H.; Wobus, U.
Submitted to the EMBL Data Library, December 1992
A:Description: Sucrose synthase expression patterns in developing seeds of Vicia faba ir
A:Reference number: S31479

A;Accession: S31479

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-806 <HEI>

C;Cross-references: EMBL:X69773; NID:g22037; PIDN:CAA49428.1; PID:g22038

C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

C;Keywords: glycosyltransferase; hexosyltransferase

F;279-753/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

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Query Match          69.84; Score 2944.5; DB 2; Length 806;
Best Local Similarity 68.8; Pred. No. 6.4e-189;
Matches 549; Conservative 122; Mismatches 126; Indels 1; Gaps 1;

QY 3 HASGDRVEDTLHAHRELVALLSKYVNGKGILOPHIL-----DALDEVQSGGRALAEGLD 62
DB 10 HSLREDELTANREILALLSRIEAKGKGILOHQHVIAPFEIPENRQKLTGDAFGE 69

QY 63 VLSAQEAIPLPFAVAIAVPRGWEYVRVNVVHLSVEQLTVSEYLRFKBEELVDGQHND 122
DB 70 VLSAQEAIPLPFAVAIAVPRGWEYVRVNVVHLSVEQLTVSEYLRFKBEELVDGQHND 129

QY 123 PYVLELDFEFPNVSVPRNRSSSIGNGVQVFLNRHLSIMFRNRCLEPLDLFLGRHKG 182
DB 130 NFVLELDFEFPTAFPRPTLNKSGNGVQVFLNRHLSAKLFHDKESLHPLEFLRLHSYKG 189

QY 183 HVMNMDRIOSLQSLQSVLTKAEHLSKLPADTPYSQFAYKFOEWGLEKMGDTAGHVLE 242
DB 190 KTMMDRIQNPDSLOHLVAKSEYLSVDPETPYSEFHFQBEIGLERGMGDSAEVLE 249

QY 243 MIHLDDIIQAPDPSTSEKELGRIPMFNVVWSPHGYFGQANVLGLPDGTGGQIVYILDQ 302
DB 250 SIQLLDLLLEAPDPSTSEKELGRIPMFNVVWSPHGYFGQANVLGLPDGTGGQIVYILDQ 309

QY 303 VRLAENEMVLRLKQGLDVSFKILIVTRLIPDAKGTSCNQRLEKISGTQHTYILRVPRN 362
DB 310 VRLAENEMVLRLKQGLDVSFKILIVTRLIPDAKGTSCNQRLEKISGTQHTYILRVPRN 369

QY 363 ENGLKKNISRFDPVWVPLETFAEDAAGEIAAELOGTDFDIIIGNYSDGNLVASILSYKGI 422
DB 370 QKGIWKWISRFDPVWVPLETFAEDAAGEIAAELOGTDFDIIIGNYSDGNLVASILSYKGI 429

QY 423 TQCNIAHALEKTYKPSDIPFKNFDEKHYFSCQFTADIIAMNADFIIITSTYQBIAGSKN 482
DB 430 TQCNIAHALEKTYKPSDIPFKNFDEKHYFSCQFTADIIAMNADFIIITSTYQBIAGSKN 489

QY 483 TVQYQESHTAFTLPGLYRVVHGIDVPDKFNIVSPGADMSIYFPHTKAKRLTSLHSGIE 542
DB 490 TVQYQESHTAFTLPGLYRVVHGIDVPDKFNIVSPGADMSIYFPHTKAKRLTSLHSGIE 549

QY 543 NLIYDPEONDEHIGLHDDRSPKILFPMARLDVRKNITGLVEAFKAKCLRELNLVAVAG 602
DB 550 ELLYSTVENEHICVLDKDRSPKILFPMARLDVRKNITGLVEAFKAKCLRELNLVAVAG 609

QY 603 YNDVNKSKDEEIAEIEKMHLEIKTHMLFGQFRWISAOQTNRAENGELRYIADTCHGAFVQ 662
DB 610 -DRKESKDLLEAKEMKMYELIETKNGQFRWISAOQTNRAENGELRYIADTCHGAFVQ 668

QY 663 PALYAEPLTVEAMTGLPFTFATLHGGPABIIIEHGVSGFHIDPHYEPQAVNLMAFPDR 722
DB 669 PALYAEPLTVEAMTGLPFTFATLHGGPABIIIEHGVSGFHIDPHYEPQAVNLMAFPDR 728

QY 723 CKQDPDHWNVISAGLQRIYKTYKLYSER-XTLAGVYGFVKVSKLELTRYLEMF 782
DB 729 VKADPDSHMDKISLQGLQRIEYKTYKLYSERLTLAGVYGFVKVSKLELTRYLEMF 788

QY 783 YILKRELAKTVPLAIDQ 800
DB 789 YALKYKLAESVPLAVZE 806

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RESULT 11

S32451

sucrose synthase (EC 2.4.1.13) Ss2 - barley

```

C;Species: Hordeum vulgare (barley)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C;Accession: S32451; S31501
R;Martinez de Ilarduya, O.; Vicente-Carabajosa, J.; Sanchez de la Hoz, P.; Carbonero, P.
FEBS Lett. 320, 177-181, 1993
A;Title: Sucrose synthase genes in barley. cDNA cloning of the Ss2 type and tissue-speci-
C;Keywords: glycosyltransferase; hexosyltransferase
F;284-758/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
A;Reference number: S32451; MUID:93209382; PMID:8458435
A;Accession: S32451
A;Molecule type: mRNA
A;Residues: 1-816 <MAR>
A;Cross-references: EMBL:X69931; NID:g19059; PIDN:CAA49551.1; PID:g19100
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;284-758/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
F;106,129,146,417,589,640/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match          69.34; Score 2922; DB 2; Length 816;
Best Local Similarity 68.14; Pred. No. 2.1e-187;
Matches 546; Conservative 114; Mismatches 132; Indels 10; Gaps 4;

QY 3 HASGDRVEDTLHAHRELVALLSKYVNGKGILOPHIL-----DALDEVQSGGRALAE 58
DB 14 HSVRERIGHLSAHTNELVAFTSELVNGKGMLOPHQITABYNAAIPAE---REKLKNT 70

QY 59 PELVLSAQEAIPLPFAVAIAVPRGWEYVRVNVVHLSVEQLTVSEYLRFKBEELVDG 118
DB 71 PFEDLLGAGAIPLPFAVAIAVPRGWEYVRVNVVHLSVEQLTVSEYLRFKBEELVDG 130

QY 119 QHNDPYVLELDFEFPNVSVPRNRSSSIGNGVQVFLNRHLSIMFRNRCLEPLDLFLRGH 178
DB 131 STDNPFVLELDFGFPNASFPRLSKSGINGVQVFLNRHLSKLFHDKESYELNLFRAH 190

QY 179 RHKGHVMMDRIOSLQSLQSVLTKAEHLSKLPADTPYSQFAYKFOEWGLEKMGDTAG 238
DB 191 NYKGMTVMMDRIOSLQSLQSVLTKAEHLSKLPADTPYSQFAYKFOEWGLEKMGDTAG 250

QY 239 HVLMIHLDDIIQAPDPSTSEKELGRIPMFNVVWSPHGYFGQANVLGLPDGTGGQIVY 298
DB 251 RASTIHLDDLLLEAPDPSSLEKFLGTIPMVNVVILSPHGYFAQANVLGPDGTGGQIVY 310

QY 299 ILDOVRALENEMVLRLKQGLDVSFKILIVTRLIPDAKGTSCNQRLEKISGTQHTYILRV 358
DB 311 ILDOVRALENEMVLRLKQGLDVSFKILIVTRLIPDAKGTSCNQRLEKISGTQHTYILRV 370

QY 359 PFRNENGLKKNISRFDPVWVPLETFAEDAAGEIAAELOGTDFDIIIGNYSDGNLVASILSY 418
DB 371 PFKTEDIKKNISRFDPVWVPLETFAEDAAGEIAAELOGTDFDIIIGNYSDGNLVASILSY 430

QY 419 KMGITQCNIAHALEKTYKPSDIPFKNFDEKHYFSCQFTADIIAMNADFIIITSTYQBI 478
DB 431 KMGITQCNIAHALEKTYKPSDIPFKNFDEKHYFSCQFTADIIAMNADFIIITSTYQBI 490

QY 479 GSKNTVQYQESHTAFTLPGLYRVVHGIDVPDKFNIVSPGADMSIYFPHTKAKRLTSLH 538
DB 491 GSKNTVQYQESHTAFTLPGLYRVVHGIDVPDKFNIVSPGADMSIYFPHTKAKRLTSLH 550

QY 539 GSIENLADPEONDEHIGLHDDRSPKILFPMARLDVRKNITGLVEAFKAKCLRELNLVAV 598
DB 551 TEIEELLFQONDEHIGLHDDRSPKILFPMARLDVRKNITGLVEAFKAKCLRELNLVAV 610

QY 599 VVAGYNDVNK-SKDRREIAEIEKMHLEIKTHMLFGQFRWISAOQTNRAENGELRYIADTH 657
DB 611 VVAGYNDVNK-SKDRREIAEIEKMHLEIKTHMLFGQFRWISAOQTNRAENGELRYIADTH 668

QY 658 GAFVQPALYAEPLTVEAMTGLPFTFATLHGGPABIIIEHGVSGFHIDPHYEPQAVNLMA 717
DB 669 GAFVQPALYAEPLTVEAMTGLPFTFATLHGGPABIIIEHGVSGFHIDPHYEPQAVNLMA 728

QY 718 DFFDRCKQDPDHWNVISAGLQRIYKTYKLYSERLTLAGVYGFVKVSKLELTRYLE 777
DB 729 DFFDRCKQDPDHWNVISAGLQRIYKTYKLYSERLTLAGVYGFVKVSKLELTRYLE 788

QY 778 YLEMFYILKRELAKTVPLAID 799

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Db 789 YLEMYALKYRKAAATVPLAVE 810
 RESULT 12
 S37560
 sucrose synthase (EC 2.4.1.13) - carrot
 C:Species: Daucus carota (carrot)
 C:Date: 09-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C:Accession: S37560
 R:Sturm, A.
 submitted to the EMBL Data Library, October 1993
 A:Description: Nucleotide sequence of a cDNA clone coding for sucrose synthase from carrot
 A:Reference number: S37560
 A:Accession: S37560
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-808 <STU>
 A:Cross-references: EMBL:X75332; NID:g406316; PIDN:CAA53081.1; PID:g406317
 C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
 C:Keywords: glycosyltransferase; hexosyltransferase
 F:281-755/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
 Query Match 69.0%; Score 2910.5; DB 2; Length 808;
 Best Local Similarity 67.8%; Pred. No. 1.2e-186;
 Matches 542; Conservative 114; Mismatches 141; Indels 3; Gaps 2;
 Db 3 HASGDRVEDTLAHNRNELVALLSKYVNGKGLQPHHILDALDEVQSGGRAL--AEGPF 60
 10 HSLREMDSTLANHRNEILMRLSRIESHGKGLKPHQLLAEYEAISKEDKXLDGCGAF 69
 61 LDVLSAQAEIVLPPTVAIVRPPGWVYRVNVHLSVEQLTVSEYLFKKEELVDGQH 120
 70 AEVKTQAEIVSPWVALAIRLPGWVEYRVNVHLSVEQLTVSEYLFKKEELVIGSS 129
 121 NPYVLELDFEPPNVGVPNRRSSSINGVQFNLRLSSIMFNRNCEPLDPLFLGRHR 180
 130 DANFVLELDFAPTAFFPRTLTSGINGVEFLNRHLSAKMFGKDSMHLEFLRLNY 189
 181 KGVMMNLNRIOQLGRLOSLVTKAEHLSKLPADTPYSQPAYKFOEWGLKKGMDTAGV 240
 190 NGKTLMLNRRVNVNGIQLMLRAGDYLSTLPSDTPYSEFEHFKFOETGFERGMDTAERV 249
 241 LEMHLLDIIQAPDPSLTLEKELGRIPMIVNVVSPHGYFGQANVLGLDTCQIVYL 300
 250 TEMFHLDDLEAPDASTLTFTLGKIPWVNVVLSPHGYFAENVLYGYPDTGGQVYL 309
 301 DQVRALENEMVLRKXQGLDVSFKILITVRLIPDAKGTSCNORLERISGTQHYILRVPF 360
 310 DQVVALEREMIKKEQGLDIPKRLIVTRLLPDAVGTTCNQRLKVFYGAZHAHLRVPF 369
 361 RNENGILKMWISRFVWPVYLETFAADMAEIAELQCTPPIIGNYSDGNLVASLLSYKM 420
 370 RTEKGILRWISRFVWPVYLETETEDVAKEIALELQAKPDIIIGNYSEGNLVASLLAHKL 429
 421 GITQCNIAHALEKTKYDSDIPKMRDEKHFSCQPTADIIAMNADPILITSTYQETAGS 480
 430 GVYQCTIAHALEKTKYDSDIYMEKFDKKYHFSQCTADIIAMNADPILITSTYQETAGS 489
 481 KNTVGQVESHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPFTEKAKRLTSLHGS 540
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 541 IENLIYDPEQNDHEIGHLLDRSKPILFSMAKRLDRVQNTGLVEFAKAKRLRELNVLYV 600
 550 IEELLYSSVNEEHLCKIKDKNKPILFTMARLDNVKNTLGFVEVYAKSPKRLVNLVYV 609
 601 AGYNDVNNKDRREIAEIEYKMHLEIKTNHLEFGQFRTISAQTNARNKELYIADTHGAF 660
 610 GG-DRRKESKDLBEQAQKKMYELIDYKLVNGQFRTISSQNNVRNRELVAIADTYGAF 668
 661 VQPALYEAFTLVVEAMTCGLPTFATLHGGAFAEIEHGVSGFHLDPYHPQAVNLMADFF 720

Db 669 VQPAFYEAFTLVVEAMTCGLPTFATLHGGAFAEIIVHGKSGPHIDPHGGEQVAELLVNF 728
 QY 721 DRCKODPDHWNISGAGLQRIYKTYTWKYSERLMTLAGVYGFVKVSKLERLETRYLE 780
 Db 729 EKCKTDPQMDALSAGLAKRIQEKYTWQIYSERLLTLAGVYGFVKHVKSLDRLEIRYLE 788
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 Db 789 MFYALKYRKLAESVPLAKDE 808
 RESULT 13
 T49233
 sucrose synthase-like protein - Arabidopsis thaliana
 N:Alternate names: Protein F7K15.40
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
 C:Accession: T49233
 R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeidler, K.; Mewes, H.W.; Rudd, S.; Len
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25019
 A:Accession: T49233
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-808 <OBE>
 A:Cross-references: EMBL:AL353871; GSPDB:GN00061; ATSP:F7K15.40
 A:Experimental source: cultivar Columbia; BAC clone F7K15
 C:Genetics:
 A:Gene: ATSP:F7K15.40
 A:Map position: 3
 A:Introns: 35/2; 128/2; 192/3; 304/3; 336/3; 394/3; 433/3; 489/2; 564/2; 752/2; 798/3
 C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
 Query Match 68.9%; Score 2904.5; DB 2; Length 808;
 Best Local Similarity 68.3%; Pred. No. 3e-186;
 Matches 545; Conservative 112; Mismatches 140; Indels 1; Gaps 1;
 QY 3 HASGDRVEDTLAHNRNELVALLSKYVNGKGLQPHHILDALDEVQSGGRALAEAGPFLD 62
 Db 12 HSQERLDATLVAQKNEVFALLSRVEAKGKGLQHHQIIAEFEAMPLETQKLGKGAFFE 71
 QY 63 VLSAQAEIVLPPTVAIVRPPGWVYRVNVHLSVEQLTVSEYLFKKEELVDGQND 122
 Db 72 FLRSQAQAEIVLPPTVAIVRPPGWVYRVNVHLSVEQLTVSEYLFKKEELVDGKNG 131
 QY 123 PYVLELDFEPPNVGVPNRRSSSINGVQFNLRLSSIMFNRNCEPLDPLFLGRHKG 182
 Db 132 NFTLELDFEPPNAAFPRTLUNKYIGGVFEFLNRHLSAKLFADKESLHPLXFLHSHSG 191
 QY 183 HVMMNLNRIOQLGRLOSLVTKAEHLSKLPADTPYSQPAYKFOEWGLKKGMDTAGHVL 242
 Db 192 KTLMLNRRVNVNGIQLMLRAGDYLSTLPSDTPYSEFEHFKFOETGFERGMDTAERV 251
 QY 243 MIHLLDIIQAPDPSLTLEKELGRIPMIVNVVSPHGYFGQANVLGLDTCQIVYLQ 302
 Db 252 MIRLLDLEAPDPTLENFLGRIPMIVNVVLSPHGYFAENVLYGYPDTGGQVYLQ 311
 QY 303 VRALENEMVLRKXQGLDVSFKILITVRLIPDAKGTSCNORLERISGTQHYIILRVFPN 362
 Db 312 VRALETMLQRIKQGLNITPRILITRLPDAAGTTGQRLKVKYGSQYCDILRVFRT 371
 QY 363 ENGLKMWISRFVWPVYLETFAADMAEIAELQCTPPIIGNYSDGNLVASLLSYKMI 422
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 QY 423 TQCNIAHALEKTKYDSDIPKMRDEKHFSCQPTADIIAMNADPILITSTYQETAGS 482
 Db 432 TQCTIAHALEKTKYDSDIYWKLDKYPHFSQCTADIIAMNADPILITSTYQETAGS 491
 QY 483 TVGQYSSHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPFTEKAKELTSLHGS 542
 Db 492 TVGQYSSHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFAYTEKRLTAFHLE 551

Db 191 NNRVQTVNC:QDLRLRIAGBYLSKLPDSPTYSDEPHKFEQIBPGRGWGDTAERHSEMFHML 250
Qy 248 LDI IQAPDPSTLEKFLGRIPMIENVVVVSPHGYFGQANVGLPDTGGQIVYILDQVRALE 307
Db 251 LLLLEAPDACLTEFLGKIPMIENVVVILSPHGYFAQENVLGYVDTGGQVYVYILDQVPAME 310
Qy 308 NEMVLELKKQGLDVSPKILIVLRIIPDANKTSCNQLERISGTOHTYILRVPERNENGIL 367
Db 311 REMTKRIKQSGLDIIPRIILVTRLLPDVAGTTCNLRLEKVFGEAHSKILRVPRTEKGIL 370
Qy 368 KXWISRFDPVWPLYLEFAEDAAGEIAAEALQCTPDIIGNYSDGNLVSALLSYKMGITQCNI 427
Db 371 RKWISRFVWPFVWETTEDVAKELALELAKXPDLLIGNYSEGNLVSALLANKLGVTOCTI 430
Qy 428 AHALEKTKPDSDFWKNFDEKHYFSCQFTADTIANNNADFIITSTYQEIAGSKNTVGQY 487
Db 431 AHALEKTKPDSDIYWEKEDKHYFSSQFTADLIAMNHTDFIITSTFQEIAGSKDITVGQY 490
Qy 488 ESHTAFTLPLRYVVEGIDVDPKENVISPGADMSIVFPHTEKAKRLTSLHGSIEHLIYD 547
Db 491 ESHTAFTMPGLYRVVHGIDVDPKENVISPGADTSVYFYTEKKRLTALHPEDILFS 550
Qy 548 PEONDEHIGHLDRSPILFSMARLDRVKNITGLVEAFKCAKRLBLVNLVVVAGYNDVN 607
Db 551 SVENKEHICVLKORYXPILFTMARLDNVKNLTGLVEWYAKPKLRLVNLVVVGG-DRRK 609
Qy 608 KSKOREEIAEIEKQHELIKTHNLFGQFRNISAQTNRNAGELYRYIADTHGAFVQPALYE 667
Db 610 ESKOLEQAQMKKNGYGLIDTYKINGOFNISAQKNRVNRNGELYRCIADTKGAFVQPAFYE 669
Qy 668 AGLTVVEAMTCGLPTFATLHGGAETIEHGVSGEHLDPYHPOAVNLMAFFDRCKQDP 727
Db 670 AGLTVVEAMTCGLPTFATLHGGAETIEHGVSGEHLDPYHPOAVNLMAFFDRCKQDP 729
Qy 728 DHWNISAGLQRIYKYTWKIYSERIMTLAGVYGFWKYVSKLERLETRRYLEMEFYIKF 787
Db 730 SHWETISAGLKRQEKYTWQIYSERILTLGGVYGFWKVSKLDRIRIRYLEMEFCALKY 789
Qy 788 RELAKTVPLAID 799
Db 790 RNLAESVPLAID 801

Search completed: May 24, 2004, 11:25:38
Job time : 19.424 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 19.4153 seconds
(without alignments)
2132.550 Million cell updates/sec

Title: US-10-080-114A-2

Perfect score: 4217

Sequence: 1 STHASGURVEDTLHAHREL.....YILKRELAKTVPLAIDQPQ 802

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pep:*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3158	74.9	766	2	US-08-553-436A-8
2	2879.5	68.3	805	4	US-09-598-401C-77
3	1833	43.5	806	4	US-08-684-005-2
4	467.5	11.1	720	4	US-09-394-272-14
5	466.5	11.1	1083	4	US-09-394-272-11
6	450	10.7	1056	4	US-09-394-272-1
7	447.5	10.6	963	4	US-09-394-272-12
8	447.5	10.6	963	4	US-09-394-272-13
9	445	10.6	1059	4	US-09-394-272-5
10	444	10.5	1068	2	US-08-429-054A-11
11	444	10.5	1068	2	US-08-718-777-7
12	444	10.5	1068	3	US-09-051-341-7
13	444	10.5	1068	4	US-09-394-272-8
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17	438	10.4	1054	2	US-08-778-656-4
18	436.5	10.4	1053	4	US-09-394-272-6
19	425	10.1	1054	4	US-09-394-272-3
20	420	10.0	1059	4	US-09-697-367-16
21	414	9.8	1057	4	US-09-697-367-23
22	414	9.8	1057	4	US-09-394-272-2
23	411	9.7	1057	3	US-08-853-948B-2
24	408.5	9.7	1081	4	US-09-394-272-4
25	401.5	9.5	1084	4	US-09-394-272-9
26	396	9.4	846	1	US-08-356-354-2
27	396	9.4	846	2	US-08-778-656-2

28	351	8.3	1049	4	US-09-394-272-10	Sequence 10, Appl
29	342	8.1	125	4	US-09-598-401C-76	Sequence 76, Appl
30	307	7.3	908	1	US-08-356-354-6	Sequence 6, Appl
31	307	7.3	908	2	US-08-778-656-6	Sequence 6, Appl
32	280	6.6	668	4	US-09-697-367-2	Sequence 2, Appl
33	262.5	6.2	368	4	US-09-697-367-24	Sequence 24, Appl
34	256	6.1	343	3	US-08-853-948B-10	Sequence 10, Appl
35	251	6.0	341	3	US-08-853-948B-4	Sequence 4, Appl
36	233.5	5.5	365	4	US-09-697-367-8	Sequence 8, Appl
37	222	5.3	343	3	US-08-853-948B-3	Sequence 3, Appl
38	221	5.2	348	3	US-08-853-948B-5	Sequence 5, Appl
39	172	4.1	210	4	US-09-697-367-10	Sequence 10, Appl
40	161	3.8	507	4	US-09-134-001C-3978	Sequence 3978, Ap
41	160.5	3.8	358	4	US-09-697-367-20	Sequence 20, Appl
42	155	3.7	59	3	US-09-125-984-2	Sequence 2, Appl
43	152.5	3.6	502	4	US-09-134-001C-4511	Sequence 4511, Ap
44	149.5	3.5	369	4	US-09-543-681A-7514	Sequence 7514, Ap
45	148	3.5	393	4	US-09-252-991A-19043	Sequence 19043, A

ALIGNMENTS

RESULT 1

US-08-553-436A-8

: Sequence 8, Application US/08553436A

: Patent No. 5866790

: GENERAL INFORMATION:

: APPLICANT: HESSE, Holger

: APPLICANT: MULLER-KOBER, Bernd

: TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

: TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE

: TITLE OF INVENTION: CONCENTRATION

: NUMBER OF SEQUENCES: 8

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen

: STREET: 1180 Avenue of the Americas

: CITY: New York

: STATE: NY

: COUNTRY: US

: ZIP: 10036-8403

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent in Release #1.0, Version #1.30

: CURRENT APPLICATION DATA: US/08553.436A

: APPLICATION NUMBER: US/08553.436A

: FILING DATE: 17-NOV-1995

: CLASSIFICATION: 800

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: PCT/EP94/01671

: FILING DATE: 20-MAY-1994

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: DE P 4317596.1

: FILING DATE: 24-MAY-1993

: ATTORNEY/AGENT INFORMATION:

: NAME: Meilman, Edward

: REGISTRATION NUMBER: 24,735

: REFERENCE/DOCKET NUMBER: P/951-117

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (212) 382-0700

: TELEFAX: (212) 382-0888

: TELEX: 236925

: INFORMATION FOR SEQ ID NO: 8:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 766 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: protein

: US-08-553-436A-8

Query Match 74.9%; Score 3158; DB 2; Length 766;

[illegible]

RESULT 2

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US-09-598-401C-77
? Sequence 77, Application US/09598401C
? Patent No. 6596925
? GENERAL INFORMATION:
? APPLICANT: Perera, J. Ranjan
? APPLICANT: Eagleton, Claire
? APPLICANT: Rice, Stephen J.
? TITLE OF INVENTION: Compositions and Methods for the
? TITLE OF INVENTION: Modification of Gene Expression
? FILE REFERENCE: 11000.1036C2
? CURRENT APPLICATION NUMBER: US/09/598,401C
? CURRENT FILING DATE: 2000-06-20
? PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/246,591
? PRIOR FILING DATE: 1999-07-30
? PRIOR APPLICATION NUMBER: PCT/NZ00/00018
? PRIOR FILING DATE: 2000-02-24

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RESULT 3

US-08-684-005-2

```

: PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/27/96, 599
: PRIOR FILING DATE: 1999-03-25
: NUMBER OF SEQ ID NOS: 120
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 77
: LENGTH: 805
: TYPE: PRT
: ORGANISM: Eucalyptus grandis
: US-09-598-401C-77

Query Match      68.3%; Score 2879.5; DB 4; Length 805;
Best Local Similarity 67.1%; Pred. No. 6.7e-259;
Matches 536; Conservative 119; Mismatches 141; Indels 3; Gaps 2

QY  2  THASGRVEDTLHAHNNELVALLSKYVKNKGILQPHIILDALDEVQSGGRALAEPPFL 61
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  9  SHSLRELDETLSAHRNDIIVAFLSVEAKKGILQHQIFAETFAISEESRAKLDDGAFG 68
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  62 DVLRSAQEAIVLPFPVAIAVRPPGVMYVYRVNVNHELVSQLTIVSEYLRKFKEELVDGQHN 121
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  69 EVLKSTQEALIVSPWALAVRPPGWEHTRVNVHALVLEQLEVAEYVHFKEELADGSLN 128
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  122 DPVYELDFEPPNVSVPRNRRSSIGNGVQFTLNHRHSSIMFRNRCDCLEPLDIFLRGHRHK 181
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  129 GNFVLEDFEPTTASFPRTLSKSGNGVEFLNRHLSAKLFDHKESLHPLLEFLQVHCYK 188
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  182 GHVWMLNDRIQSRLGRISVLTAKAEHLSEKLPADTPYSQAFKFOEWGLKXMGDTAGHVL 241
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  189 GKMMYNNAIRIQNFSQHVLRKABEYLTSLKPTPYSQFBEKFQEIGLERGWGDTAERVL 248
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  242 EMTHLLDITIAQDPDSTLEKFLGRIPMIFNVWVSPHGYPQANVLGLPDTGGQIVTILD 301
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  249 EMTQLLLDLEAPDPCLEKFLDRVPMFNVVIMSPHGYPADQDVLGYPDTGGQVWYILD 308
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  302 QVRALLENWVLRLKKQGLDVSPKILIVTRLIPDAKGTSCNORLBRISGTQHTYILRVPPFR 361
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  309 QVRALBEEMLHRTIKQGLDITPRILITRLLPDAVGTTCQRLKEKVFTEYSHILRVPPFR 368
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  362 NENGILKKMISRPDVPAPYLTETAEADAAGTAAEHLQGTDPDFLIGNYSGNVASILLSKQG 421
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  369 NEGVVKKMISRFEPWPYLERIYETDVASELAELQGPDLILIGNYSGNIVASLHAKIG 428
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  422 ITQCNTAHALEKTKYPTDSITFWKNDFEKYHFSQCFADIIAMNADFIITSTYQEIAGSK 481
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  429 VTQCTIAHALEKTKYTESDIYMKKEEKYHFSQCFADLIAMNHTDFTITSTFQEIAGSK 488
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  482 NTVGQVESHATAFTPLGLYRVVHGIDVPDPKENVISPGADMSTIYPHTEKAKGLTSIHGSI 541
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  489 DTVGQVESHNNFTPLGLYRVVHGIDVPDPKENVISPGADMSTIYPAYTEQERLRSFHPET 548
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  542 ENLIYDPEQNDHEIGHLDDRSKPLFSMAELDRVKNITGLVEAPAKCAKRELNVNLVVA 601
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  549 EELLFSDVENKEHLCVLKDKKKPIIFTMARLDRVKNITGLVEWVGKSKRELANLVVG 608
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  602 GYNDVVK- SKOREIEAIEKQHELKITHNLI FCGPRWTISAQTNARNGELVRYIADTHGAF 660
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  609 G--DRRKDSKULSEQEMKKNYDLIEKYKLGQFPRWISSQGMARVRNGELVRYICTDKGVF 666
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  661 VQPALYEAFCGLTVVEAMTCGLPTFATLHGSPARTIEHGVSFGLDPPVHPEQAVNLMDFF 720
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  667 VQPAIYEAFCGLTVVEAMTCGLPTFATCNGGPAELIVHGKSGYHIDLPFHGQAAELLVDFF 726
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  721 DRCKQDPDHWNVNSGAGLQRIYEKYTWKIVSEIRMTLAGYVGVKYYSKLERLTRYLE 780
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  727 NKCKIDQSHWDELISKGMQRIEKYTWKIVSERLLNLTAVYGVGMKHTVNLDRRESRYLE 786
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  781 MFVILKFRSLAKTWPLAID 799
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  787 MFYALKYRPLAOSVPPAVE 805
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 3

US-08-684-005-2

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; Sequence 2, Application US/08684005
; Patent No. 682918
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Buikema, William J.
; APPLICANT: Bauer, Christopher C.
; TITLE OF INVENTION: BACTERIAL SUCROSE SYNTHASE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,005
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARSB:508
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-684-005-2

Query Match 43.5%; Score 1833; DB 4; Length 806;
Best Local Similarity 45.6%; Pred. No. 1.9e-161;
Matches 359; Conservative 163; Mismatches 251; Indels 14; Gaps 7;

QY 17 RNELVALLSKYVNGKXGILPHHLDALDVGSGGREALAEGPDL---VLSAQAELVL 73
DB 14 KHLRGEISLROODKNYLLRNLDILNVYAEYCKQKQKPSYKPSNLSKLIYYTQRIQS 73

QY 74 PPFVAIVAPRPGVMEYVRVNVVHLSVEQLTVSEYLFKKEELVDGQNDPY---VLELDF 130
DB 74 DSNFCFIIRPKIAAQEYVRLTA-DLDVEPMVQCELLDRORLVNKEH--PYEGDILELDF 130

QY 131 EPNVSVPRNRSSTGNGVQFLNRHLSSIMFR-NRDCLEPLDPLFLCHRRHKGHWMLND 189
DB 131 GPFCYDPTTRDPKNGIKGVQYLNRYLSKLFQDSQQWLESFNFRLNHYNGIQLINH 190

QY 190 RIGSLGRQLSVLTKAEHLKLPADTPYSOFAYKFEWGLEKGWGTAGHVLMIHLLD 249
DB 191 QIOSQOOLSOQVKNALNFVSDRNPDEYFRLOQTMTGPFPGMGTASVRDTINILDE 250

QY 250 IIQAPDPTLEKFLGRIPMIFNVVSPHGVFGQANVLGPDGTGGQIVYLQVRALENE 309
DB 251 LIDSPDQTLAEAFISRIPIFRIVLNSAGHFGQGVLRGPDGTGGQVYVLDQAKNLEKQ 310

QY 310 M---VLRKFKQGLDVPKILIVTRLIPDAKGTSCNQLERISGTHYILRVPPRNN-G 365
DB 311 LQEDAILAGLEVLNVQPKVILTRLIENSQTLNCRLEKVGYGTEANWILRVLPREFNPK 370

QY 366 ILKKWISRFVWPVLYETFAEDAAGEIAELQCTPDFLIIGNVSDGNLVSLSYKMGITQC 425
DB 371 MTQNWISRFVWPVLYETFAIDSERELLAEFGRPDLIVNGYTDGNLVAFLLTIRMKVYTC 430

QY 426 NIAHALEKTKYPSDIFWKNFDEKYPHPSQFTADIIAMNADFIITSTYQEIAGSKNTVG 485

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RESULT 4

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US-09-394-272-14
; Sequence 14, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Synecchocystis sp.
; US-09-394-272-14

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Query Match 11.1%; Score 467.5; DB 4; Length 720;
Best Local Similarity 27.5%; Pred. No. 2.1e-34;
Matches 145; Conservative 108; Mismatches 190; Indels 85; Gaps 20;

QY 272 VVVVSPHGYGQANV-LGL-PDTGGQIVYLQVRALE-ENEMVLRLKKQGLDVPKILIV 328
DB 8 ILLISVHGLRGENLELRGDRADTGGQYKYLELALVKNPQVARVD-----LL 56

QY 329 TRLIPDAKGTSCNQLERISGTHYILRVPPRNNGLKKWISRFVWPVLYETFAEDA 388
DB 57 TRLIKDPKVADYAPRELIG-DRAQIVRISCGPEEYIAKEML-----WDYLDNFA-DHA 109

QY 389 GSIAELQGTPDFTIIGNVSDGNLVSLSYKMGITQCNIHAL---EKTYPDSDFMKN 445
DB 110 LDYLKEQPELPDVTSHSVADAGYVGTSLSHQLGIPLVHTGHSLSGRSKRLLSGIKADE 169

QY 446 FDEKHPSCQFTADIIAMNADFIITSTYQEIAGSKNTVGQYESHATFLPCLRVVHGI 505
DB 170 IESRYNMARRINAEETIGSAARVITSTHQIA-----EQYAQY----- 208

QY 506 DVFDPP-KENIVSPGADMSIYFPHTKAKRLTSLHGSINLIYDPEQNDHIGHLDNRKCP 564
DB 209 DYOQDQXVLVPPGTDLDEKYP-PKGNWEWETPIVQELQRFDRHPR-----XP 254

QY 565 ILFSMARLDRVKNITGLVEAPAKCAKRLVNLVVVAGYNDVNKSKOREIAEI-----E 619

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Db 255 IILASRPDPKRNTHUKLIAAQQSPQQAQANLVIVAG-----NRDDITDLDQGP 306
Qy 620 KQHELIXT---HNFGQPRWTSQOTNRARN-GELYRYIADTHGAFVQVOPALYAEAFGLTVVE 675
Db 307 VLTDLTLLTIDRYLXGKWAY--PKQQAEDVVALFRLTALSQGVFINPALTPEFGLTIE 364
Qy 676 AWTGCLPTFATLHGCPARIIEHGVSGFHDVHPQAVNLMDAFDRCKQDPDHWVNISG 735
Db 365 AARGGVPAVATEDGDFVDIINKCONGYLINPLDEVD----IADKLVKNDKQKQOFUSE 420
Qy 736 AGLQRIYKTYKTYSERLMTLAGYGVFWKYSKLERLETRYLEWFI 783
Db 421 SGLEGVKHYSPVSEVY--LEAINALTQTSVLKRSDLKERRTLYY 466

RESULT 5
US-09-394-272-11
; Sequence 11, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-394-272-11

Query Match 11.1%; Score 466.5; DB 4; Length 1083;
Best Local Similarity 24.3%; Pred. No. 5.2e-34;
Matches 184; Conservative 130; Mismatches 285; Indels 159; Gaps 32;

Qy 111 FKELVDG-QHNDPVYLEDFFPNVSPRNRSSI-----GNGVQLP 153
Db 67 FVEEVNSPDSLYK-TLKIATRNTRERSNRLENICAKIWLARKKQIVMDDGVLRS 126
Qy 154 NRELSSIMPRNDCLEPILDEL-RGRHKGHWMLNDR-QSLGRLOSVLTKAEHLKLP 212
Db 127 KRRIEBOEN-DAEEDLLSELSEGEKOK-----NDGEKSESVVTTLEPPRDHMPRIR 179
Qy 213 ADTPYSQPAYKFOEWLEKMGWGTAGHLEMIHLDDIIQAPDPSTLEKFLGRIPMFNV 272
Db 180 SE-----NQIWEED-----DKSSR-----NLYIVLRQVEIGFSDLF-----VFENM 216
Qy 273 VV-----VSPHGYF-GQANVLGL-PDTGGQIVY-LDQVRALENMVLRLLK 316
Db 217 LVGLTWCLYLVPCFTNCSMEGLVRGENMELGRDSTGGQVYVWELARALAN-----T 269
Qy 317 QGLDVSPKLIIVTRLPDAK-GTSCNQRLEIS---GTQH---TYILVRPERNENGILKK 363
Db 270 EGVH---RDVLTQRISSPEVDYSYGEPEVMVSCPPESGSDSCSYIIRIPC-----GSRDK 322
Qy 370 WISRPDVPVYLETFAEDAAGEIAA-----SQG-----TPDFIIGNYSDGNLVASLLSY 418
Db 323 YIPKESLWPHIPFVDGALNHIYSIARSLGEQVNGKPIWPYVIGHYADAGEVAHAHLG 382
Qy 419 KMGITQCNIAHALEKTYK----PDSDFWKNFDEKHFSCQFTADIIAMNADFIITSTY 474
Db 383 ALNVMPVLTGSLGRNKFQELLOQGRITREDIDRTYKIMRIEAEQSLDAEAMVVTSTR 442
Qy 475 QETAGSNVTVQYESTAFITPLGLYRVVHGIDV-----FDPKFNIV 515
Db 443 QEID-----AQW-----GLY---DGFDFKLEKLVRRRRGVSCIGRYMPRWVI 484
Qy 516 SPGADMSIYPPH--TEKAKRLTSLHGSINENLIYDPEQN--DEHIGLDDRSKPLFSMAR 571
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Db 485 PPGMDFSVVLTQDSQEPDGLKSLIGPDRNQIKKVPPIWSEIMRFFSNPHKPTILALSR 544
Qy 572 LDRVKNITGLVEAPAKAKLRELNVVVVAGVNDVKNKSDREIEAIEKMHKHLKTHNLP 631
Db 545 PDHKKNVTTLVKAFCGCPRLRELANLVILGNRDDIEEPPNSSSVVLVNMVLLDQDYDY 604
Qy 632 GQFRWISAQTNARNGELRYIADTHGAFVQVOPALYAEAFGLTVVEAMTCGLPTPATLHGCP 691
Db 605 GQVAY-PKHQKQSEVPDIYRLAAKTGVFINPALVEPGLTILIEAAAYGLPIVAITN3GF 663
Qy 692 AEIIIEHGVSGEHIIDPHYPEQAVNLMDAFDRCKQDPDHWVNISGAGLQRIYKTYKTY 751
Db 664 VDIVKALNGLLADP-HDQQAII---SDALLX-LVANKHLWAECKKNGLKNIH-RFSWPEHC 718
Qy 752 ERLMTLAGYGVFWKYSKLERLETRYLEWFI 789
Db 719 R-----NYLSHVEHCRNRHP*SSLDIMKVP 744

RESULT 6
US-09-394-272-1
; Sequence 1, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-394-272-1

Query Match 10.7%; Score 450; DB 4; Length 1056;
Best Local Similarity 26.4%; Pred. No. 1.7e-32;
Matches 145; Conservative 97; Mismatches 218; Indels 90; Gaps 18;

Qy 272 VVVSPHGYF-GQANVLGL-PDTGGQIVYLDQVRALENE-----MYLRLKQGLDV 321
Db 176 VVLSLHGLIRGENNELGRDSTGGQVYVWELARALGSMGPYRVYDILLTRQVSAPEGVW 235
Qy 322 S---PKILIVTRLPDAKGTSCNQRLEISGTQHTYILRVPPFRNENGILKKNISFEDVWP 378
Db 236 SYGEP-----TEMLSRNSENSTELGESSG---AVIIRIPF-----GPKDKYVAKELLWP 283
Qy 379 YLETRADAAG-----EIAAELQTPDPIIGNYSDGNLVASLLSYKMGITQCNI 427
Db 284 TYPEFDGALSHITKQMSKVLGEQIGGGLPWVPSVHGRYADAGDSALLSGALNVPMVFT 343
Qy 428 AHALEKTK---YPSDITFWKFNDEKHFSCQFTADIIAMNADFIITSTYQEIAGSKNT 483
Db 344 GHSIGRDKLDQLLKQGRLSREVDATYKIMRIEAEELCLDASEIYVITSTROBIEBQ--- 400
Qy 484 VQYESHTAFTPLGLYRVVHGIDV-----FDPKFNIVSPGADMSIY 524
Db 401 -----WQLYHGFDLVLERKLARMRRGVSGHGRFMPRMKIPPGMBFNHI 445
Qy 525 FPHTEKAKRLTSLHGSIE-NLIYDPEQNDEHIGLDDRSKPLFSMARLDVRNITGLVE 583
Db 446 AP---EDADMDTIDGKHESNANPDPIVWSEIMRFFSNGRKPMILALARPPEKNLITLVK 503
Qy 584 APAKAKLRELNVVVVAGVNDVKNKSDREIEAIEKMHKHLKTHLFGQFRWISAQTNR 643
Db 504 AFGECPRLRELANTLIIIGNRDDIDEMSTSSSVLSILKLDKYDLYGQVAY-PKHQK 562
Qy 644 ARNGELRYIADTHGAFVQVOPALYAEAFGLTVVEAMTCGLPTPATLHGCPAIEIIEHGVSGFH 703
```


530 KAKRLTSLHSGSIENLIYDPEONDEHIG-----HLDKRSKPIILFSMAR 571
1: : : : :
449 -----EDIDGSDVKDIDVGLGASPKSMPIWAEVVRFLTNPKHMLALS 496
1: : : : :
572 LDRVKNITGLVEAPAKCAKRELNLVAVAGYNDVNSKDBEEIABIEKHMLIKTNL 631
1: : : : :
497 FDPKKNITTLVKAFGECPRLANLTLIMGNRDDIDMSAGNASVLTTLKLDIKYDLY 556
1: : : : :
632 GQFRWISAOQNRANGELYRIADTHGAFVOPALYEAFLTVVEAMTGLPTFATLHGGP 691
1: : : : :
557 GSVAF-PKHNNQADVPEIYRLAAKMGVFINPALVEPPGLTLIAAAHGLPIVATKNGGP 615
1: : : : :
692 AEIIEHGVSGFHIDPYHPEQAVNLMADEFFDRCKQDPDHVNVNISGAGLQRIYEKTYWKIYS 751
1: : : : :
616 VDIITNALNGLLVDPHQ-----NAIADALLKLVADKKNLWQECRNGRLNIH-LYSWPEHC 670
1: : : : :
752 ERLMT-LAGVYGFWMKYVSKLERLSTRYLE 780
1: : : : :
671 RYTLTRVAGC-----RLRNPRLK 689
1: : : : :
RESULT 11
US-08-718-777-7
; Sequence 7, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
; APPLICANT: Van Asseche, C.
; APPLICANT: Lando, D.
; APPLICANT: Bruneau, J. M.
; APPLICANT: Voelker, T.
; APPLICANT: Gervais, M.
; TITLE OF INVENTION: MODIFICATION OF SUCROSE
; TITLE OF INVENTION: PHOSPHATE
; TITLE OF INVENTION: SYNTHASE IN PLANTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Barbara Rae-Venter
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,777
; FILING DATE: NOT YET ASSIGNED
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,471
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.072.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-777-7

Query Match 10.5%; Score 444; DB 2; Length 1068;
Best Local Similarity 25.2%; Pred. No. 6.3e-32;
Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 234 GDTAGHVLEMIHLLDIIOAPDPSTLEKFLGRIPMI-----FNVVVVSPHGYP- 281
1: : : : :
DB 141 GDTIGEL-----APVEITKKFQNFSDLTWSDDNKSKGLYVILSVHGLVR 188
1: : : : :
QY 282 QGANVLGH-PDTGGQIVYLDOVRALENEMVRLKKQGLDVP---KILIVTRLI--PD- 334
1: : : : :
DB 189 GENMELGRSDSTGGQYKVVELARA-----MSMMPGVYRVLDLFTROVSSPDV 235
1: : : : :
QY 335 -----AKGTSCNORLERISGTQHTYILRVPERNENIGILKKWISRRFDPVPLETF 383
1: : : : :
DB 236 DWSGEPTMELCAGSDGEGMGESG---AYIVRIPC-----OPRDKYLKKEALWPLQSF 288
1: : : : :
QY 384 AEDAAGEI-----AAELQGT-----PDFIIGNYDGNLVAALLSYKMGITQCNIAHALE 432
1: : : : :
DB 289 VDGALAHILNMSKALGEQVGNRGPVLPYVIHGHYADAGDVAALLSGALNVPMLTCHSLG 348
1: : : : :
QY 433 KTK-----YDSDIDFWNDFEKHFSCQFTADIANNADFIITSTYQEIAGSKNTVGGYE 488
1: : : : :
DB 349 RNKLEQLLKQGRMSKBEIDSTYKIMRIEGEBELADASELVITSTQEID-----EQW- 401
1: : : : :
QY 489 SHTAFTLPLGLYRVVHGDV-----FDPKFNIVSPGADMSIYFPHTE 529
1: : : : :
DB 402 -----GLY---DGFVKLEKVLARARRGVSCHGRYMPRMVVPDGMDFSNVVH-- 448
1: : : : :
QY 530 KAKRLTSLHSGSIENLIYDPEONDEHIG-----HLDKRSKPIILFSMAR 571
1: : : : :
DB 449 -----EDIDGSDVKDIDVGLGASPKSMPIWAEVVRFLTNPKHMLALS 496
1: : : : :
QY 572 LDRVKNITGLVEAPAKCAKRELNLVAVAGYNDVNSKDBEEIABIEKHMLIKTNL 631
1: : : : :
DB 497 FDPKKNITTLVKAFGECPRLANLTLIMGNRDDIDMSAGNASVLTTLKLDIKYDLY 556
1: : : : :
QY 632 GQFRWISAOQNRANGELYRIADTHGAFVOPALYEAFLTVVEAMTGLPTFATLHGGP 691
1: : : : :
DB 557 GSVAF-PKHNNQADVPEIYRLAAKMGVFINPALVEPPGLTLIAAAHGLPIVATKNGGP 615
1: : : : :
QY 692 AEIIEHGVSGFHIDPYHPEQAVNLMADEFFDRCKQDPDHVNVNISGAGLQRIYEKTYWKIYS 751
1: : : : :
DB 616 VDIITNALNGLLVDPHQ-----NAIADALLKLVADKKNLWQECRNGRLNIH-LYSWPEHC 670
1: : : : :
QY 752 ERLMT-LAGVYGFWMKYVSKLERLSTRYLE 780
1: : : : :
DB 671 RYTLTRVAGC-----RLRNPRLK 689
1: : : : :
RESULT 12
US-09-051-341-7
; Sequence 7, Application US/09051341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,341
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.072.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-051-341-7

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; APPLICATION NUMBER: US 08/549,016
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,200
; FILING DATE: 12-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Vetter, Ph.D.,
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.110.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-051-341-7

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Query Match      10.5%; Score 444; DB 3; Length 1068;
Best Local Similarity 25.2%; Pred. No. 6.3e-32;
Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 234 GTAGHVLEMIHLLDIIQAPDPSTLEKFLGRIPMI-----FNVVVSPHGYE- 281
Db 141 GTIGEL-----APVETTKKFORNFSDLTWSDDNKEKKLVILVLSVHGLVR 188

QY 282 GQANVLGL-PTGGQIVYILDQVRALLENEMVLKKGGLDVP---KILIVTRLI--PD- 334
Db 189 GENMELGRSDTGGQVKYVVELARA-----MSMPGVYRVDLFTQVSSPDV 235

QY 335 -----AKGTSNORLERISGTQHTYILRVFRNENGILKKWISRFDPWPLYLTF 383
Db 236 DWSYGEPTMLCAGSDGCMGSGG---AYIVRIPC-----GPRDKYLKKEALWPLYLQEF 288

QY 384 AEDAAGEI-----AAELQGT-----PDFIIGNYSDGNLVASLLSYKMGITOCNIAHALE 432
Db 289 VQALAHILMSKALGEQVNGEPVLPYVTHGYADAGVAALLSGALNVPMVLTGHSLG 348

QY 433 KTK-----YPDSDFMKNFDEKHFSQFTADIAMNADFIITSTQEIAGSKNTVGQYE 488
Db 349 RNKLEQLLKQGRMSKEEIDSTYKIMRRIEGEELALDASELVITSTRQID-----EQW- 401

QY 489 SHTAFTPLGLYRVVHGIDV-----DGFVVKLEKVLARARRGVSGHRYMRMVVIPPGMDFSNVVVH-- 529
Db 402 -----GLY---DGFVVKLEKVLARARRGVSGHRYMRMVVIPPGMDFSNVVVH-- 448

QY 530 KAKRLTSLHGSITENLYDPEQNDHEIG-----HLDERSKPIILFSMAR 571
Db 449 -----EDIDGDGVKDDIVGLEGASPKSMPTIWAETVWRFLTNPKPMILALS 496

QY 572 LDRVKNITGLVEAFKAKLRELNVLVVAGYNDVKNKSDREIEAEIKMHELKITHNLF 631
Db 497 PDPKKNITTLVKAFCGRPLRELANTLIMGNRDDIDDMASAGNASVLTTLVKLIDKYDLY 556

QY 632 GQFRWLSAQTNRARNGELYRIADTHGAFVQPALYEAFGLTVVEAMTCGLPTATLHGGP 691
Db 557 GSVAF-PKHNNQADVPEITYKLAAMKGVFINPALVEPFGLTIEAAHAGLPVATKNGGP 615

QY 692 AEIIEHGVSGFHIDPYHPEQAVNLMADEFDRCKQDPDHWNINISGAGLQRIYEKYITWKIYS 751
Db 616 VDTITNALNGLLVDPHDQ-----NAIADALLKLVADKNLMQECRRNGLRNIH-LYSWPEHC 670

QY 752 ERLMT-LAGVYGFWKVKYVKLERLETRRYLE 780
Db 671 RTYLTRVAGC-----RLRNPRWLK 689

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RESULT 13
US-09-394-272-8
; Sequence 8, Application US/09394272
; Patent No. 6472588

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; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1068
; TYPE: PRT
; ORGANISM: Zea mays
US-09-394-272-8

Query Match      10.5%; Score 444; DB 4; Length 1068;
Best Local Similarity 25.2%; Pred. No. 6.3e-32;
Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 234 GTAGHVLEMIHLLDIIQAPDPSTLEKFLGRIPMI-----FNVVVSPHGYE- 281
Db 141 GTIGEL-----APVETTKKFORNFSDLTWSDDNKEKKLVILVLSVHGLVR 188

QY 282 GQANVLGL-PTGGQIVYILDQVRALLENEMVLKKGGLDVP---KILIVTRLI--PD- 334
Db 189 GENMELGRSDTGGQVKYVVELARA-----MSMPGVYRVDLFTQVSSPDV 235

QY 335 -----AKGTSNORLERISGTQHTYILRVFRNENGILKKWISRFDPWPLYLTF 383
Db 236 DWSYGEPTMLCAGSDGCMGSGG---AYIVRIPC-----GPRDKYLKKEALWPLYLQEF 288

QY 384 AEDAAGEI-----AAELQGT-----PDFIIGNYSDGNLVASLLSYKMGITOCNIAHALE 432
Db 289 VQALAHILMSKALGEQVNGEPVLPYVTHGYADAGVAALLSGALNVPMVLTGHSLG 348

QY 433 KTK-----YPDSDFMKNFDEKHFSQFTADIAMNADFIITSTQEIAGSKNTVGQYE 488
Db 349 RNKLEQLLKQGRMSKEEIDSTYKIMRRIEGEELALDASELVITSTRQID-----EQW- 401

QY 489 SHTAFTPLGLYRVVHGIDV-----DGFVVKLEKVLARARRGVSGHRYMRMVVIPPGMDFSNVVVH-- 529
Db 402 -----GLY---DGFVVKLEKVLARARRGVSGHRYMRMVVIPPGMDFSNVVVH-- 448

QY 530 KAKRLTSLHGSITENLYDPEQNDHEIG-----HLDERSKPIILFSMAR 571
Db 449 -----EDIDGDGVKDDIVGLEGASPKSMPTIWAETVWRFLTNPKPMILALS 496

QY 572 LDRVKNITGLVEAFKAKLRELNVLVVAGYNDVKNKSDREIEAEIKMHELKITHNLF 631
Db 497 PDPKKNITTLVKAFCGRPLRELANTLIMGNRDDIDDMASAGNASVLTTLVKLIDKYDLY 556

QY 632 GQFRWLSAQTNRARNGELYRIADTHGAFVQPALYEAFGLTVVEAMTCGLPTATLHGGP 691
Db 557 GSVAF-PKHNNQADVPEITYKLAAMKGVFINPALVEPFGLTIEAAHAGLPVATKNGGP 615

QY 692 AEIIEHGVSGFHIDPYHPEQAVNLMADEFDRCKQDPDHWNINISGAGLQRIYEKYITWKIYS 751
Db 616 VDTITNALNGLLVDPHDQ-----NAIADALLKLVADKNLMQECRRNGLRNIH-LYSWPEHC 670

QY 752 ERLMT-LAGVYGFWKVKYVKLERLETRRYLE 780
Db 671 RTYLTRVAGC-----RLRNPRWLK 689

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RESULT 14
US-08-553-436A-6
; Sequence 6, Application US/08553436A
; Patent No. 5866790
; GENERAL INFORMATION:
; APPLICANT: HESSE, Holger
; APPLICANT: MULLER-ROBER, Bernd
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

```

TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
TITLE OF INVENTION: CONCENTRATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553.436A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/01671
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA: DE P 4317596.1
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-436A-6

Query Match 10.5%; Score 441.5; DB 2; Length 1045;
Best Local Similarity 26.8%; Pred. No. 1e-31;
Matches 146; Conservative 102; Mismatches 130; Indels 107; Gaps 24;
QY 272 VVVSPHGYE-GQANVLGL-PTDGGQIVYILDQVRALENE-----MVLRLKKQGLDV 321
DB 163 LVLSLHGLRGENNELGRSDTGGQYVVELARALGSMGPGYVRVDLLTRQVSSPDVW 222
QY 322 S---PKLIVTRLPDAKGTSCNQLRERISGTQHTYILRVPPFRNENGILKKWISRPDVP 378
DB 223 SYGTEMLNPR--DSNGFDDDD--DEMGSAGYIVRIPF-----GPRDKYIAKEELWP 273
QY 379 YLETFADAGEIA-----AELOQT-----PDIIGNYSDGNLVSLLSKYKGTQCN 427
DB 274 YIPEFVDGALNHVQMSKVILGEQIGSGETWPVVAIGHYADAGSAAALLSGLVNPMLLT 333
QY 428 AHAEKTKYPD-----SDIFWKNFDEKYHFSCOPTADIIAMNADFIITSTYQEIA 478
DB 334 CHSLGRDKLEQLLKQGRMSKDDI-----NNTYKIMRRIEAEELSLSLDAEIVITSTROEIE 388
QY 479 GSKNTVQYQESHFTAPLGL-----YRVVHGIDV---FDPKFNIVSPCADMSIYFPHTK 530
DB 389 -----EQWHLVDGFD-PVLERKLARMKRGVSCYGRFPMRMVVIIPGMEFNHIVPH--- 438
QY 531 AKRLTSLHSGIENLIYDPEQNDH-----IGHLDDRSKPIFLFSMARLDVRKNI 578
DB 439 -----EGDMCG---ETEETEHTSPDPPIWAEIMRFPFSKPKRMILALARPDPKNI 488
QY 479 TGLVEAFKAKAKRELNVVAVAGYNDVNKSKDREELAEIEKHELIKTHNLFGQFRWIS 530
DB 389 -----EQWHLVDGFD-PVLERKLARMKRGVSCYGRFPMRMVVIIPGMEFNHIVPH--- 438
QY 531 AKRLTSLHSGIENLIYDPEQNDH-----IGHLDDRSKPIFLFSMARLDVRKNI 578
DB 439 -----EGDMCG---ETEETEHTSPDPPIWAEIMRFPFSKPKRMILALARPDPKNI 488
QY 579 TGLVEAFKAKAKRELNVVAVAGYNDVNKSKDREELAEIEKHELIKTHNLFGQFRWIS 638
DB 489 TTVKAFGECPRLRELNLTLIMGNRDGIDEMSSSTSSSVLLSVLKLIDQYDLGQVAY-P 547

QY 639 AQTNRANGELYRYIADTHGAFVOPALYEAGLTVVEMTCGLFTFATLHGSPAILIEHG 698
DB 548 KHKQADVPETIYRLAAKTGKVFINPAFIEPFGTLIEAAAHGLPMVATKNGPVDIOQVL 607
QY 699 VSGPHIDPYHQAV-----NLMADE--FFDRCQDDPDHVVNISGAGLORIEKYTWKYS 751
DB 608 DNGLLVDP-HEQQSIIATALLKLVDKQIWTKCOQN-----GLKNIH-LYSWPHS 655
QY 752 ERLMT 756
DB 656 KTYLS 660
RESULT 15
US-09-394-272-7
; Sequence 7, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-394-272-7
Query Match 10.5%; Score 441.5; DB 4; Length 1045;
Best Local Similarity 26.8%; Pred. No. 1e-31;
Matches 146; Conservative 102; Mismatches 190; Indels 107; Gaps 24;
QY 272 VVVSPHGYE-GQANVLGL-PTDGGQIVYILDQVRALENE-----MVLRLKKQGLDV 321
DB 163 LVLSLHGLRGENNELGRSDTGGQYVVELARALGSMGPGYVRVDLLTRQVSSPDVW 222
QY 322 S---PKLIVTRLPDAKGTSCNQLRERISGTQHTYILRVPPFRNENGILKKWISRPDVP 378
DB 223 SYGTEMLNPR--DSNGFDDDD--DEMGSAGYIVRIPF-----GPRDKYIAKEELWP 273
QY 379 YLETFADAGEIA-----AELOQT-----PDIIGNYSDGNLVSLLSKYKGTQCN 427
DB 274 YIPEFVDGALNHVQMSKVILGEQIGSGETWPVVAIGHYADAGSAAALLSGLVNPMLLT 333
QY 428 AHAEKTKYPD-----SDIFWKNFDEKYHFSCOPTADIIAMNADFIITSTYQEIA 478
DB 334 CHSLGRDKLEQLLKQGRMSKDDI-----NNTYKIMRRIEAEELSLSLDAEIVITSTROEIE 388
QY 479 GSKNTVQYQESHFTAPLGL-----YRVVHGIDV---FDPKFNIVSPCADMSIYFPHTK 530
DB 389 -----EQWHLVDGFD-PVLERKLARMKRGVSCYGRFPMRMVVIIPGMEFNHIVPH--- 438
QY 531 AKRLTSLHSGIENLIYDPEQNDH-----IGHLDDRSKPIFLFSMARLDVRKNI 578
DB 439 -----EGDMCG---ETEETEHTSPDPPIWAEIMRFPFSKPKRMILALARPDPKNI 488
QY 579 TGLVEAFKAKAKRELNVVAVAGYNDVNKSKDREELAEIEKHELIKTHNLFGQFRWIS 638
DB 489 TTVKAFGECPRLRELNLTLIMGNRDGIDEMSSSTSSSVLLSVLKLIDQYDLGQVAY-P 547
QY 639 AQTNRANGELYRYIADTHGAFVOPALYEAGLTVVEMTCGLFTFATLHGSPAILIEHG 698
DB 548 KHKQADVPETIYRLAAKTGKVFINPAFIEPFGTLIEAAAHGLPMVATKNGPVDIOQVL 607
QY 699 VSGPHIDPYHQAV-----NLMADE--FFDRCQDDPDHVVNISGAGLORIEKYTWKYS 751
DB 608 DNGLLVDP-HEQQSIIATALLKLVDKQIWTKCOQN-----GLKNIH-LYSWPHS 655

QY 752 ERLMT 756
: :
Db 656 KYLS 660

Search completed: May 24, 2004, 11:28:51
Job time : 22.4153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 53.2675 Seconds

(without alignments)
4254.056 Million cell updates/sec

Title: US-10-080-114a-2

Perfect score: 4217

Sequence: 1 STHASGRVDTLHARNEL.....YILKRELAKTVPLAIDPQ 802

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4217	100.0	802	5	Aae28499 Corn sucr
2	4177	99.1	809	5	Aae28502 Corn Sus3
3	3456	82.0	809	5	Abb92810 Herbicida
4	3158	74.9	766	2	Aar66222 Sucrose-s
5	3126	74.1	797	6	Abr39586 A. thalia
6	3105.5	73.6	805	5	Abb93752 Herbicida
7	3105.5	73.6	805	6	Abr39585 A. thalia
8	3049.5	72.3	773	5	Aae28503 Maize suc
9	2993.5	71.0	802	5	Aae28500 Corn sucr
10	2990.5	70.9	808	3	Aay85664 Rice sucr
11	2985	70.8	816	5	Aae28501 Corn sucr
12	2974	70.5	816	7	Adc07856 Rice prot
13	2974	70.5	816	7	Adc08209 Rice prot
14	2964.5	70.3	815	7	Adc68460 Lolium pe
15	2961	70.2	806	5	Aau97898 Cotton su
16	2960	70.2	814	7	Adc68366 Lolium pe
17	2934	69.6	816	7	Adc68367 S. arundi
18	2924.5	69.4	808	7	Adc68459 Lolium pe
19	2920.5	69.3	808	7	Adc68364 Lolium pe
20	2916.5	69.2	808	5	Abg69063 Amino aci
21	2914.5	69.1	771	3	Aay85666 PS3 prot
22	2906.5	68.9	808	7	Adc68365 S. arundi
23	2904.5	68.8	808	5	Abb92501 Herbicida
24	2879.5	68.3	805	3	Aab16282 Eucalyptu
25	2879.5	68.3	805	3	Aab16336 Eucalyptu

ALIGNMENTS

RESULT 1

AAE28499
ID AAE28499 standard; protein; 802 AA.

XX AC AAE28499;

XX DT 27-DEC-2002 (first entry)

XX DE Corn sucrose synthase (Sus3).

XX KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
cellulose; corn; Sus3.

XX OS Zea mays.

XX PN WO200267662-A1.

XX PD 06-SEP-2002.

XX PF 21-FEB-2002; 2002WO-US005137.

XX PR 22-FEB-2001; 2001US-0270777P.

XX (PION-) PIONEER HI-BRED INT INC.

XX PI Dhugga KS, Helentjaris TG, Niu X;

XX DR WPI; 2002-691625/74.

XX DR N-PSDB; AAD45849.

XX PT New polynucleotide and its encoded sucrose synthase, useful for
modulating the level of sucrose synthase in transgenic plants (e.g. maize
or soybean) to improve stalk length, reduce grain breakage, or improving
plant or grain strength.

XX PS Claim 12; Page 103-104; 125pp; English.

XX CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
constitutive sucrose synthase (Sus1) and their corresponding nucleic
acids. The polynucleotide, or its encoded protein, is useful for
modulating the level of sucrose synthase in a transgenic plant.
XX CC increasing cellulose production in the stalk tissue of a transgenic
plant, or increasing the concentration of cellulose in the tissues of a
seed of a transgenic plant. This is particularly useful in plant (e.g.
maize or soybean) breeding, especially for e.g. improving stalk length in
maize, reducing grain breakage during combining, transport or movement
into storage, or improving plant or grain strength. The present sequence

Aab28141 Sucrose s
Aau80753 Eucalyptu
Abb93562 Herbicida
Adc08297 Rice prot
Adc07858 Rice prot
Abb91573 Herbicida
Adc07862 Rice prot
Abb93633 Herbicida
Adc07860 Rice prot
Adc07854 Rice prot
Aaw53103 Anabaena
Abg69054 Amino aci
Aab16313 Pinus rad
Abg69052 Amino aci
Aab16309 Eucalyptu
Aab16312 Pinus rad
Aay85667 Plant col
Aab16284 Pinus rad
Abm73686 DNA clone
Aab16314 Pinus rad

26 2879.5 68.3 805 3 AAB28141
27 2879.5 68.3 805 5 AAU80759
28 2867.5 68.0 808 5 ABB93562
29 2755.5 65.3 777 7 ADC08297
30 2755.5 65.3 777 7 ADC07858
31 2340.5 55.5 942 5 ABB91573
32 2319.5 55.0 786 7 ADC07862
33 2296 54.4 843 5 ABB93633
34 2248.5 53.3 798 7 ADC07860
35 1971 46.7 514 7 ADC07854
36 1833 43.5 806 2 AAW53103
37 1692.5 40.1 395 5 ABG69054
38 1212 28.7 348 3 AAB16313
39 802.5 19.0 225 5 ABG69052
40 709 16.8 149 3 AAB16309
41 635 15.1 217 3 AAB16312
42 623 14.8 198 3 AAY85667
43 622 14.7 158 3 AAB16284
44 615 14.6 204 7 ABM73686
45 587 13.9 139 3 AAB16314

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CC is corn Sus3 protein
XX Sequence 802 AA;
SQ

Query Match 100.0%; Score 4217; DB 5; Length 802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 802; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STHASGRVEDTLHAHRELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEPPF 60
DB 1 STHASGRVEDTLHAHRELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEPPF 60

QY 61 LQVLSAQEAIVLPFVAIAVRPRGWEYRVNVVHLSVEQLTVSEYLFKKEELVDGQH 120
DB 61 LQVLSAQEAIVLPFVAIAVRPRGWEYRVNVVHLSVEQLTVSEYLFKKEELVDGQH 120

QY 121 NDPVYLELDFEPENSVPRNRSSTGNGVQFLNRHLSSIMFRNRDCLPFLDRLGRHR 180
DB 121 NDPVYLELDFEPENSVPRNRSSTGNGVQFLNRHLSSIMFRNRDCLPFLDRLGRHR 180

QY 181 KGHVMMNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWDTAGHV 240
DB 181 KGHVMMNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWDTAGHV 240

QY 241 LEMIHLLDIIQAPDPSTLEKFLGRIPMIFNVVVSPHGYFGQANVLGLPDTGQIYVIL 300
DB 241 LEMIHLLDIIQAPDPSTLEKFLGRIPMIFNVVVSPHGYFGQANVLGLPDTGQIYVIL 300

QY 301 DQVRALENMWLRKKQGLDVSPKILIVTRLIPDAKGTSCNQRLEISGTQHTYILRVFP 360
DB 301 DQVRALENMWLRKKQGLDVSPKILIVTRLIPDAKGTSCNQRLEISGTQHTYILRVFP 360

QY 361 RNENGLIKKWIISFDVWPYLETFAEDAAGEIAAELQTPDFIIGNYSDGNLVASLLSYKM 420
DB 361 RNENGLIKKWIISFDVWPYLETFAEDAAGEIAAELQTPDFIIGNYSDGNLVASLLSYKM 420

QY 421 GITQCINAHALEKTKYPSDSIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQEIAGS 480
DB 421 GITQCINAHALEKTKYPSDSIFWKNFDEKHFSCQFTADIIAMNADFIITSTYQEIAGS 480

QY 481 KNTVGYESHTAFTLPGLYRVHSGIDVDFPKFNIIVSGADMSIYFPHTEKAKELTSLHGS 540
DB 481 KNTVGYESHTAFTLPGLYRVHSGIDVDFPKFNIIVSGADMSIYFPHTEKAKELTSLHGS 540

QY 541 IENLIYDPEQNDHIGLDRSKPILFMSMARLDVRKNITGLVEAPAKAKLRVLNVLVY 600
DB 541 IENLIYDPEQNDHIGLDRSKPILFMSMARLDVRKNITGLVEAPAKAKLRVLNVLVY 600

QY 601 AGYNDVNKSKDREIEIAIEKMHLEIKTHNLFGQFRWISAOINARMCHELRYIADTHGAF 660
DB 601 AGYNDVNKSKDREIEIAIEKMHLEIKTHNLFGQFRWISAOINARMCHELRYIADTHGAF 660

QY 661 VQALYAEAFGLTVVEAMTCGLPTFATLHGGAPEIIEHGVSGFHDIDPVHPQAVNLMADPF 720
DB 661 VQALYAEAFGLTVVEAMTCGLPTFATLHGGAPEIIEHGVSGFHDIDPVHPQAVNLMADPF 720

QY 721 DRCKQDPDHVNIISGAGLQRIYKTYWKIYSERLMTLAGVYGVKYSKLERLETRYLE 780
DB 721 DRCKQDPDHVNIISGAGLQRIYKTYWKIYSERLMTLAGVYGVKYSKLERLETRYLE 780

QY 781 MFYILKEREIAKTIVPLAIDQFQ 802
DB 781 MFYILKEREIAKTIVPLAIDQFQ 802

RESULT 2
ID AAE28502
XX AAE28502 standard; protein; 809 AA.
AC AAE28502;
XX
DT 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)

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XX DE
XX XX
XX KW Corn Sus3-Sorghum EST chimeric protein.
XX KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX KW cellulose; corn; Sus3; chimeric.
XX OS
XX OS Zea mays.
XX OS Sorghum propinquum.
XX OS Chimeric.
XX FH Key Location/Qualifiers
XX FT 1. .13
XX FT /note= "Sorghum propinquum EST DNA encoded peptide"
XX FT 14. .809
XX FT /note= "Corn Sus3 protein"
XX FT
XX WD200267662-A1.
XX PN
XX XX 06-SEP-2002.
XX XX 21-FEB-2002; 2002WO-06005137.
XX PF
XX XX 22-FEB-2001; 2001US-0270777P.
XX PR
XX XX (PION-) PIONEER HI-BRED INT INC.
XX PA
XX XX Dhugga XS, Helentjaris TG, Niu X;
XX PI
XX XX WPI; 2002-691625/74.
XX DR N-PSDB; AAD45856.
XX XX
XX PT New polynucleotide and its encoded sucrose synthase, useful for
XX PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX PT or soybean) to improve stalk length, reduce grain breakage, or improving
XX PT plant or grain strength.
XX PS Claim 12; Page 120-121; 125pp; English.
XX CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX CC acids. The polynucleotide, or its encoded protein, is useful for
XX CC modulating the level of sucrose synthase in a transgenic plant,
XX CC increasing cellulose production in the stalk tissue of a transgenic
XX CC plant, or increasing the concentration of cellulose in the tissues of a
XX CC seed of a transgenic plant. This is particularly useful in plant (e.g.
XX CC maize or soybean) breeding, especially for e.g. improving stalk length in
XX CC maize, reducing grain breakage during combining, transport or movement
XX CC into storage, or improving plant or grain strength. The present sequence
XX CC is Corn Sus3-Sorghum EST chimeric protein. (Updated on 29-AUG-2003 to
XX CC standardise OS field)
XX SQ Sequence 809 AA;

Query Match 99.1%; Score 4177; DB 5; Length 809;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 DRYEDTTHAHNELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEPPDLVRS 66
DB 14 DRYEDTTHAHNELVALLSKYVNGKGIQPHHILDALDEVQSGGRALAEPPDLVRS 73

QY 67 AQEAIVLPFVAIAVRPRGWEYRVNVVHLSVEQLTVSEYLFKKEELVDGQNDPVYL 126
DB 74 AQEAIVLPFVAIAVRPRGWEYRVNVVHLSVEQLTVSEYLFKKEELVDGQNDPVYL 133

QY 127 ELDFEPENSVPRNRSSTGNGVQFLNRHLSSIMFRNRDCLPFLDRLGRHRKHVMM 186
DB 134 ELDFEPENSVPRNRSSTGNGVQFLNRHLSSIMFRNRDCLPFLDRLGRHRKHVMM 193

QY 187 LNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWDTAGHVLEIHL 246
DB 194 LNDRIQSLGRLOSLVTKAEHLSKLPADTPYSQFAYKFOEWGLEKGGWDTAGHVLEIHL 253

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QY 247 LLDIIQAPDSTLEKFLGRIPMFNVVSPHGYFGQANVLGLPDTGGQIYVILDOVRAL 306
 DB 254 LLDIIQAPDSTLEKFLGRIPMFNVVSPHGYFGQANVLGLPDTGGQIYVILDOVRAL 313
 QY 307 ENEMWLRLKKQGLDVSPKILVTRLIIDAKGTCNQRLERISGTHQHYILRVPPRNENGI 366
 DB 314 ENEMWLRLKKQGLDVSPKILVTRLIIDAKGTCNQRLERISGTHQHYILRVPPRNENGI 373
 QY 367 LKKWISRFVWPVLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITOCN 426
 DB 374 LKKWISRFVWPVLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITOCN 433
 QY 427 IAHALEKTKYDSDIIFWKNFDEKHFSCQFTADIIAMNNADFIITSTYQBIAGSKNTVQ 486
 DB 434 IAHALEKTKYDSDIIFWKNFDEKHFSCQFTADIIAMNNADFIITSTYQBIAGSKNTVQ 493
 QY 487 YESHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSIEMLIY 546
 DB 494 YESHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSIEMLIY 553
 QY 547 DPEQNDHGHILDDRSKPIILFWMARLDVRVXITGLVEAFKAKRLHVLNLYVYVAGYNDV 606
 DB 554 DPEQNDHGHILDDRSKPIILFWMARLDVRVXITGLVEAFKAKRLHVLNLYVYVAGYNDV 613
 QY 607 NKSQDREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRIADTHGAFVQOPALY 666
 DB 614 NKSQDREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRIADTHGAFVQOPALY 673
 QY 667 EAFGLTVVEAMTCGLPTFATLHGGPABIEIHGVSGFHIDPYHPEQAVNLMAADFDRCKQD 726
 DB 674 EAFGLTVVEAMTCGLPTFATLHGGPABIEIHGVSGFHIDPYHPEQAVNLMAADFDRCKQD 733
 QY 727 PDHWNISGAGLORIYKTYWISERIMTLAGYVGFWKYVSKLERLETRRYLEMFIYK 786
 DB 734 PDHWNISGAGLORIYKTYWISERIMTLAGYVGFWKYVSKLERLETRRYLEMFIYK 793
 QY 787 FRELAKTVPLAIDQP 802
 DB 794 FRELAKTVPLAIDQP 809

RESULT 3

AB892810 standard; protein; 809 AA.

AC AB892810;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 2021.

DE Herbicidal; plant; agriculture; herbicide.

KW Arabidopsis thaliana.

OS W0200210210-A2.

PN 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP009892.

XX 28-AUG-2001; 2001WO-EP009892.

XX (PAB) BAYER AG.

PA Tietjen K, Weidler M;

PI WPI; 2002-269010/31.

DR Identifying plant target proteins for herbicidally active compounds,
 XX comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant

organisms.

XX Claim 5; SEQ ID NO 2021; 261pp + Sequence Listing; English.

PS The invention relates to identifying target proteins (AB890790-AB894016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides

XX Sequence 809 AA;

SQ Query Match 82.0%; Score 3456; DB 5; Length 809;

Best Local Similarity 79.9%; Pred. No. 2.2e-305;

Matches 635; Conservative 89; Mismatches 69; Indels 2; Gaps 1;

QY 7 DRVEDTLHNEHNEVALLSKYVNGKGILOPHHILDALDEVQSG--GRALAEGPFLDVL 64
 DB 14 DRVQDTLSAHEHNEVALLSYVDQKGILOPHHILDELESVIGDDETKSLSDGPFGEIL 73
 QY 65 RSAQEAIVLPFFVAIVRPRFGVMEYVRVNYVHELSVEQLTVSEYLRKFEELVGOHNDPY 124
 DB 74 KSAMEAIVVPPFVALAVRPRFGVMEYVRVNYVHELSVEQLTVSEYLRKFEELVGOHNDPY 133
 QY 125 VLELDFFPNVSPRPNRSSIGNGVQFLNHLSSIMPRNRDCLPELDFLGRHGHV 184
 DB 134 CLELDFFPNANVRPSSSSIGNGVQFLNHLSSIMPRNRDCLPELDFLGRHGHV 193
 QY 185 NMLNDRTCSGLRQSLVTKAEHLKLPADTPYSOFAYKFOEWLEKMGWDTAGHVLMI 244
 DB 194 LXLNDRTCSGLRQSLVTKAEHLKLPADTPYSOFAYKFOEWLEKMGWDTAGHVLMI 253
 QY 245 HLLADIIQAPDSTLEKFLGRIPMFNVVSPHGYFGQANVLGLPDTGGQIYVILDOVRAL 304
 DB 254 HLLADIIQAPDSTLEKFLGRIPMFNVVSPHGYFGQANVLGLPDTGGQIYVILDOVRAL 313
 QY 305 ALENEMWLRLKKQGLDVSPKILVTRLIIDAKGTCNQRLERISGTHQHYILRVPPRNENGI 364
 DB 314 ALENEMWLRLKKQGLDVSPKILVTRLIIDAKGTCNQRLERISGTHQHYILRVPPRNENGI 373
 QY 365 GILKKWISRFVWPVLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITOCN 424
 DB 374 GILKKWISRFVWPVLETFARDAAGBIAELQGTPTDFIIGNYSDGNLVALSLSYKMGITOCN 433
 QY 425 CNIAHALEKTKYDSDIIFWKNFDEKHFSCQFTADIIAMNNADFIITSTYQBIAGSKNTV 484
 DB 434 CNIAHALEKTKYDSDIIFWKNFDEKHFSCQFTADIIAMNNADFIITSTYQBIAGSKNTV 493
 QY 485 QOYSHSTAFGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSIEMLIY 544
 DB 494 QOYSHSTAFGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEKAKRLTSLHGSIEMLIY 553
 QY 545 IYDPEQNDHGHILDDRSKPIILFWMARLDVRVXITGLVEAFKAKRLHVLNLYVYVAGYNDV 604
 DB 554 IYDPEQNDHGHILDDRSKPIILFWMARLDVRVXITGLVEAFKAKRLHVLNLYVYVAGYNDV 613
 QY 605 DVNKSQDREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRIADTHGAFVQOPALY 664
 DB 614 DVNKSQDREIEAIEKMHLEIKTHNLFGQFPMISAOINRANGELYRIADTHGAFVQOPALY 673
 QY 665 LYBAPGLTVVEAMTCGLPTFATLHGGPABIEIHGVSGFHIDPYHPEQAVNLMAADFDRCKQD 724
 DB 674 LYBAPGLTVVEAMTCGLPTFATLHGGPABIEIHGVSGFHIDPYHPEQAVNLMAADFDRCKQD 733
 QY 725 QDPDHWNIISGAGLORIYKTYWISERIMTLAGYVGFWKYVSKLERLETRRYLEMFIYK 784
 DB 734 QDPDHWNIISGAGLORIYKTYWISERIMTLAGYVGFWKYVSKLERLETRRYLEMFIYK 793
 QY 785 LKFRSLAKTVPLAID 799

Db 386 TFAEDASNEISAEIQGVPNLIIGYSDGNLVSALLASKGLVIQCNIAHALEKTKYPESDI 445
 QY 442 FKNVDEKXHFSCQTAADIIANNKADFIITSTYQIAGSKNTVQYESHTAFTLGLYRV 501
 Db 446 YMRNEDKXHFSSQTAADIIANNKADFIITSTYQIAGSKNTVQYESHTAFTLGLYRV 505
 QY 502 VHGIDVDFPKFNIIVPGADMSIYFFPTEKAKELTSLHGSIEENLIYDPEQNDHIGHLDDR 561
 Db 506 VHGIDVDFPKFNIIVPGADMTIYFFSDKERRLTALHESIEELFSAGQNDHIGHLSDQ 565
 QY 562 SKPIIFSMARLDVRKXNITGLVFAFAKAKLRELINLVVAGYNDVNKSKDRBEIAIEIKM 621
 Db 566 SKPIIFSMARLDVRKXNITGLVFAFAKAKLRELINLVVAGYNDVNKSKDRBEIAIEIKM 625
 QY 622 HELIKTNLFGQPRWISAQTNRRANGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGL 681
 Db 626 HSLIEQYDLHGEFRWIAAQNRRANGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGL 685
 QY 682 PTFATLHGGPAEIIIEHGVSGFHDIDPHPEQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 741
 Db 686 PTFATLHGGPAEIIIEHGVSGFHDIDPHPEQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 745
 QY 742 YEKYTKWISERLMLTAGVYFVKVYKSKLERLETRYLEMFIYKPRELAKTVPLAIDQ 800
 Db 746 YERYTKWISERLMLTAGVYFVKVYKSKLERLETRYLEMFIYKPRELAKTVPLAIDQ 804
 RESULT 7
 ABR39585
 AC ABR39585 standard; protein; 805 AA.
 XX ABR39585;
 DT 12-JUN-2003 (first entry)
 DE A. thaliana lipid metabolism protein (LMP)-clone ID Pkl18.
 KW Lipid metabolism protein; LMP; seed storage; plant; transgenic.
 OS Arabidopsis thaliana.
 PN WO2003014376-A2.
 PD 20-FEB-2003.
 PF 12-AUG-2002; 2002WO-US025586.
 PR 10-AUG-2001; 2001US-0311414P.
 PA (BADI) BASF PLANT SCI GMBH.
 PI Mitendorf V, Haertel H, Cirpus P;
 XX WPI; 2003-256595/25.
 DR N-PSDB; AB276371.
 PT New nucleic acid molecule encoding lipid metabolism protein, useful for
 PT producing transgenic plants, for modulating seed storage compounds, e.g.
 PT lipid or fatty acid, in plants, and for evolutionary and protein
 PT structural studies.
 XX Claim 2; Fig 12B; 108pp; English.
 PS The invention relates to isolated lipid metabolism proteins (LMP) and
 CC polynucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC ABR39572-587 represent A. thaliana LMP sequences

XX Sequence 805 AA;
 SQ Query Match 73.6%; Score 3105.5; DB 6; Length 805;
 Best Local Similarity 74.3%; Fred. No. 2e-273;
 Matches 579; Conservative 97; Mismatches 98; Indels 5; Gaps 3;
 QY 24 LSKYNKGGIILQPHILDA-LDEVGSGG-RALARGPFLDLVLSAQEAIVLPFPVAIAV 81
 Db 29 LVRYVAQGGIILQSHQILDEELKTVKVDGTLEDLANKSPFKVL--QEAIVLPFPVALAI 85
 QY 82 RRRPGVWEYRVNVNHLSSVEQLTVSSYLRFKBEELVQGHNDPVLELDPEFNVSPRPN 141
 Db 86 RRRPGVWEYRVNVNHLSSVEQLTVSSYLRFKBEELVQGHNDPVLELDPEFNVSPRPN 145
 QY 142 RSSISGNGVQFENRHLSSIMERNRDLPLDFLRGHRHGHVMMNLNDRISQSLGRQSVL 201
 Db 146 RSSISGNGVQFENRHLSSIMERNRDLPLDFLRGHRHGHVMMNLNDRISQSLGRQSVL 205
 QY 202 TKAEEHLSKLPADTPYSOFAYKFEWGLEKMGDGTAGHVLMTLLDIIQAPDPSTLEK 261
 Db 206 ARAEEFLSKLPATPYSEFEFELQGMGERGWDGTAQKVMVELLDDILQAPDPSTLEK 265
 QY 262 FLGRIPMIENVVSPHGFQGNVGLDPTGQIVYILDQFALENEMVLRLKKOGLDV 321
 Db 266 FLGRIPMIENVVSPHGFQGNVGLDPTGQIVYILDQFALENEMVLRLKKOGLDV 325
 QY 322 SPKILIVTRLIPIAKGTSCNORLERISGTOHTYILRVPRFENRNGILKKMISRPDVPWYLE 381
 Db 326 IPKILIVTRLIPIAKGTSCNORLERISGTOHTYILRVPRFENRNGILKKMISRPDVPWYLE 385
 QY 382 TFAEDAAGHIAAELOQTDPDIIIGNYSDGNLVSALLASKGLVIQCNIAHALEKTKYPESDI 441
 Db 386 TFAEDAAGHIAAELOQTDPDIIIGNYSDGNLVSALLASKGLVIQCNIAHALEKTKYPESDI 445
 QY 442 FKNVDEKXHFSCQTAADIIANNKADFIITSTYQIAGSKNTVQYESHTAFTLGLYRV 501
 Db 446 YMRNEDKXHFSSQTAADIIANNKADFIITSTYQIAGSKNTVQYESHTAFTLGLYRV 505
 QY 502 VHGIDVDFPKFNIIVPGADMSIYFFPTEKAKELTSLHGSIEENLIYDPEQNDHIGHLDDR 561
 Db 506 VHGIDVDFPKFNIIVPGADMTIYFFSDKERRLTALHESIEELFSAGQNDHIGHLSDQ 565
 QY 562 SKPIIFSMARLDVRKXNITGLVFAFAKAKLRELINLVVAGYNDVNKSKDRBEIAIEIKM 621
 Db 566 SKPIIFSMARLDVRKXNITGLVFAFAKAKLRELINLVVAGYNDVNKSKDRBEIAIEIKM 625
 QY 622 HELIKTNLFGQPRWISAQTNRRANGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGL 681
 Db 626 HSLIEQYDLHGEFRWIAAQNRRANGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGL 685
 QY 682 PTFATLHGGPAEIIIEHGVSGFHDIDPHPEQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 741
 Db 686 PTFATLHGGPAEIIIEHGVSGFHDIDPHPEQAVNLMADFFDRCKQDPDHWVNIISGAGLQRI 745
 QY 742 YEKYTKWISERLMLTAGVYFVKVYKSKLERLETRYLEMFIYKPRELAKTVPLAIDQ 800
 Db 746 YERYTKWISERLMLTAGVYFVKVYKSKLERLETRYLEMFIYKPRELAKTVPLAIDQ 804
 RESULT 8
 AAE28503
 ID AAE28503 standard; protein; 773 AA.
 XX AAE28503;
 XX AAE28503;
 DT 27-DEC-2002 (first entry)
 DE Maize sucrose synthase consensus protein.
 OS Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 KW cellulose; maize.

[illegible]

Qy	483	TVGQYEGHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTKAKRLTSLHGSIE	542
Db	471	TVGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTE-SKRLTSLHPETE	529
Qy	543	NLIYVDPQNDHGHLLDRSRKPIILFSMARLDRVKNITGLVFAFAKCAKIRELVNLIWVWAG	602
Db	530	ELIYI--SENSEHKFVLD--RKPIILFSMARLDRVKNITGLVELYIGKARLURELVNLIWVWAG	585
Qy	603	YNDVWNSKDRREETAIEIBKMHLELIKTHNLFGQFRWISAOQTNARNGELYRYIADTHGAFVQ	662
		:	
Db	586	DHG---SKDREBQAEFFKKMHDLI-DYNI-GHIRWISAOQNVNRNGELYRYICTTGKAFVQ	640
Qy	663	PALYEAEGLTIVVEAMTCGLPTFATLHGSPABIIBGVSGGFPHIDYHPQCAVNLMAADFDR	722
Db	641	PAFYEAEGLTIVVEAMTCGLPTFAT-HGGSPABIIVHGVSGGFHIDPYHDKAA--LLVDFFDK	697
Qy	723	CKQDPDRHWNISGAGLQRIYEKYTWKLYSERLMTLGVYGVKVKYVKLERLETREYLEMF	782
Db	698	CKADPSHW--ISQGLQRIYEKYTWKLYSERLMTLTGVYGVKVKYVSNLERRETRILEMF	755
Qy	783	YILKFRELAKTVPLAID 799	
Db	756	YALKYRSLASTVPLAID 772	
RESULT 9			
AAE28500			
ID	AAE28500	standard; protein; 802 AA.	
AC	AAE28500;		
XX			
XX			
DT	27-JSC-2002	(first entry)	
XX			
XX		Corn sucrose synthase shrunken-1 (Sh1) protein.	
DE			
XX		Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;	
KW		transgenic plant; plant breeding; grain breakage; grain strength; enzyme;	
KW		cellulose; corn; chromosome 9.	
XX			
OS		Zea mays.	
XX			
FN	W0200367662-Al.		
XX			
PD	06-SEP-2002.		
XX			
PF	21-FEB-2002; 2002WO-US005137.		
XX			
PR	22-FEB-2001; 2001US-0270777P.		
XX			
PA	(PION-) PIONEER HI-BRED INT INC.		
XX			
PI	Drugga KS, Helentjaris TG, Niu X;		
XX			
DR	WPI; 2002-691625/74.		
DR	N-PSDB; AAD45851.		
XX			
PT	New polynucleotide and its encoded sucrose synthase, useful for		
PT	modulating the level of sucrose synthase in transgenic plants (e.g. maize		
PT	or soybean) to improve stalk length, reduce grain breakage, or improving		
PT	plant or grain strength.		
XX			
PS	Example 9; Page 108-110; 125pp; English.		
XX			
CC	The invention relates to two sucrose synthases, shrunken-1 (Sh1) and		
CC	constitutive sucrose synthase [Sus1] and their corresponding nucleic		
CC	acids. The polynucleotide, or its encoded protein, is useful for		
CC	modulating the level of sucrose synthase in a transgenic plant,		
CC	increasing cellulose production in the stalk tissue of a transgenic		
CC	plant, or increasing the concentration of cellulose in the tissues of a		
CC	seed of a transgenic plant. This is particularly useful in plant (e.g. in		
CC	maize or soybean) breeding, especially for e.g. improving stalk length in		
CC	maize, reducing grain breakage during combining, transport or movement		

Db 421 AHKLGVTQCTIAHALEKTKYNSDIYLDKEDSVQHFSCQFTADLIAMNHTDPIITSTFOE 480
 QY 477 IAGSKNTVGQYESHATATLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEKAKRLTS 536
 Db 481 IAGSKDVTGQYESHIAFTLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEADKRLTA 540
 QY 537 LHGSNIENLIYDPEQNDHEIGHLDKRSKPIILFMSMARLDRVKNITGLVEAFKAKAKRLBLVN 596
 Db 541 FHPFIEELLYSEVENDHEKFLVKDKNPIILFMSMARLDRVKNITGLVEAFKAKAKRLBLVN 600
 QY 597 LVVVAGYNDVNKSKDRBEIAIEKHBLIKTHNLFGQFRWISAOINRANGELYRYIADT 656
 Db 601 LVIWCG-DHGNQSKDRBEQAFKQYGLIDQYKLGHRWISAOINRANGELYRYIADT 659
 QY 657 HGAFOALYEAAGLTVEAMTGLFATLHGGPAELIEHGVSGPHLDVPHQAVNLM 716
 Db 660 KGVFQVAFYEAAGLTVEAMTGLFATLHGGPAELIEHGVSGPHLDVPHQAVNLM 719
 QY 717 ADFFDRCKQDPDHVWNISGAGLQRIYBKTYWKIYSERLMTLAGVYGVFKVYVSKLERLETR 776
 Db 720 VNFPECKQDSTYWDNISQGLQRIYBKTYWKIYSERLMTLAGVYGVFKVYVSKLERLETR 779
 QY 777 RYLEMFILKRELAKVTVPLAID 799
 Db 780 RYTEMFYALKYRSLASAVPLAID 802

RESULT 11
 ID AAE28501 standard; protein; 816 AA.
 AC AAE28501;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Corn sucrose synthase (Sus1).
 XX
 KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 KM transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 KN cellulose; corn; chromosome 9.
 XX
 OS Zea mays.
 XX
 PN WC200267662-A1.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US005137.
 XX
 PR 22-FEB-2001; 2001US-0270777P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Dhugga KS, Kelentjaris TG, Niu X;
 XX
 DR WPI; 2002-531625/74.
 DR
 DR N-PSDB; AAD45852.
 XX
 XX New polynucleotide and its encoded sucrose synthase, useful for
 PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
 PT or soybean) to improve stalk length, reduce grain breakage, or improving
 PT plant or grain strength.
 XX
 XX Example 9; Page 114-115; 125pp; English.
 PS
 XX
 CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
 CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
 CC acids. The polynucleotide, or its encoded protein, is useful for
 CC modulating the level of sucrose synthase in a transgenic plant,
 CC increasing cellulose production in the stalk tissue of a transgenic
 CC plant, or increasing the concentration of cellulose in the tissues of a
 CC seed of a transgenic plant. This is particularly useful in plant (e.g.
 CC maize or soybean) breeding, especially for e.g. improving stalk length in

CC maize, reducing grain breakage during combining, transport or movement
 CC into storage, or improving plant or grain strength. The present sequence
 CC is corn Sus1 protein. Corn Sus1 gene is located at chromosome 9
 XX
 SQ Sequence 816 AA;
 Query Match 70.8%; Score 2985; DB 5; Length 816;
 Best Local Similarity 69.8%; Pred. No. 1.9e-262;
 Matches 559; Conservative 106; Mismatches 128; Indels 8; Gaps 3;
 QY 3 HASGDRVEDTLHAHNEILVALLSKYVKGKGILOPHHIL----DALDEVQSGGGRALAE 58
 Db 14 HSVRERIGDLSAHNELVAVFTRILKLGKGLQPHQIIAEYNAIPEAE---REKLKDG 70
 QY 59 PFLDVLASQAIAVLPPVAVATVPRPGVWVVRVNVHLSVEQLTVSEYLFKEXELVDG 118
 Db 71 AFEDVLRAAQAIWIPVWVALAIRPGVWEVVRVNVSELAVEELRVPEYLFQFKQLVEE 130
 QY 119 QHNDPYYVLELDFEPFNVSVPFRNRSSTIGNGVQFLNRHLSSIMFRNRDCLFELDPLR 178
 Db 131 GPNNFVLELDFEPFNASFPRLSKSIGNGVQFLNRHLSSKLFHDKESMYPLANFLRAH 190
 QY 179 RHKGHVWMLNDRIOSLGRLOSVLTAKABHLKSLPADTPYSQFAYKQFQWGLEKMGDPAG 238
 Db 191 NYKGMTWMLNDRIKSLGALQALRKABEHLSTLQADTPYSEFHRFQELGLEKMGDCAK 250
 QY 239 HVLEMIHLILLDIQAPDPESTLEKELGRIPMFNVVNVVSPHGFQGANVLPDTCQIVY 298
 Db 251 RAQETIHLDDLLEAPDESTLEKELGTIPVFNVIVILSPHGFQGANVLPDTCQGVVY 310
 QY 299 ILDOVRALENEMWLRLKQGLDVSPKILIVTRILPDAKGTSCNORLERISGTHYILRV 358
 Db 311 ILDOVRAMENEMLRLKQGLDITEKILIVTRILPDAKGTTCQGLKLVKLVTEHCHILRV 370
 QY 359 PFRNENGLIKWISRFVWVPLETFAEDAAGEIAAEALQGTDPDFIIGNYSDGNLVASLSY 418
 Db 371 PFRTEINGIVRWISRFVWVPLETFTDVAHEIAGELQANPDLIIGNYSDGNLVACLLAH 430
 QY 419 KQGLTQCNIAHALEKTKYVPSDIEFKNPDEKVFHSCQFTADLIAMNADFIITSTFOEIA 478
 Db 431 KQGVTHCTIAHALEKTKYVPSDLYKVPFDEHYHSCQFTTDLIAMNHADFIITSTFOEIA 490
 QY 479 GSKNTVGQYESHATATLGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTEKAKRLTSIH 538
 Db 491 GNKDTVGQYESHMAFTWGLYRVVHGIDVDFPKFNIVSPGADLSIYFPHTEKAKRLTSIH 550
 QY 539 GSIENLIYDPEQNDHEIGHLDKRSKPIILFMSMARLDRVKNITGLVEAFKAKAKRLBLV 598
 Db 551 PEIBELLYSQENTEHKFLVNDNRKPIIFSMARLDRVKNITGLVEAFKAKAKRLBLV 610
 QY 599 VVAGYNDVNKSKDRBEIAIEKHBLIKTHNLFGQFRWISAOINRANGELYRYIADTHG 658
 Db 611 VVCG-DHGNPDKDRBEQAFKQYGLIDQYKLGHRWISAOINRANGELYRYIADTHG 669
 QY 659 AFVQFALYEAAGLTVEAMTGLFATLHGGPAELIEHGVSGPHLDVPHQAVNLMAD 718
 Db 670 AFVQFALYEAAGLTVEAMTGLFATLHGGPAELIEHGVSGPHLDVPHQAVNLMAD 729
 QY 719 PFDKCKQDPDHVWNISGAGLQRIYBKTYWKIYSERLMTLAGVYGVFKVYVSKLERLETR 778
 Db 730 PFDKCKQDPDHVWNISGAGLQRIYBKTYWKIYSERLMTLAGVYGVFKVYVSKLERLETR 789
 QY 779 LEMFYILKRELAKVTVPLAID 799
 Db 790 LEMFYILKRELAKVTVPLAID 810

RESULT 12
 ADC07856
 ID ADC07856 standard; protein; 816 AA.
 XX
 AC ADC07856;
 XX

DT 18-DEC-2003 (first entry)
 XX Rice protein sequence Seq ID122 related to grain filling.
 DE
 XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 XX WO2003000905-A2.
 XX
 XX 03-JAN-2003.
 XX
 XX 21-JUN-2002; 2002WO-1B002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX
 XX WPI: 2003-229341/22.
 DR N-PSDB; ADC07855.
 XX
 XX New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 FT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX
 XX Claim 1; SEQ ID NO 122; 130pp; English.
 XX
 XX This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences.
 XX
 XX Sequence 816 AA;
 XX
 XX Query Match 70.5%; Score 2974; DB 7; Length 816;
 XX Best Local Similarity 69.8%; Pred. No. 2e-261;
 XX Matches 557; Conservative 105; Mismatches 134; Indels 2; Gaps 2;
 XX
 QY 3 HASGDEVDTLHARHVELVALLSKYVNGKGLQPHHLDALDEVQSGGR-ALAEQFPL 61
 DB 14 HSVREIGSLSAHFNELVAVFTLRLVNGKMLQAHQIIAEYNNASREAREKLKQAFE 73
 QY 62 DVLRSQAELVLPFPFAIAVRPGVWVYRVNVELSVFQLTVSEYLRKELVDGQHN 121
 DB 74 DVLRSQAEGIVISFWALAIRPGVWYRVNVELAVELLTVPEVLQKEQIVEGTN 133
 QY 122 DPVLELDFFPNVSPRNRSSIGNGVQFLNHRHSSIMFRNDCLEPLDLFLGRHRHK 181
 DB 134 NNFVLELDFFPNASFRPSLSKISGNVQFLNHRHSSKLFHDKESMYPLNFLRAHNYK 193
 QY 182 GHVWMLNDRISQSLGRISVLTKEAHEHLSKLPADTPYSQPAYKQFQEWLEKVGWGDAGHVL 241
 DB 194 GXTTMLNDRIRSLAQALRKAEHLISGLSADTPYSEPHRFTQELGLEKVGWGDCAKRSQ 253

QY 242 SMHLLDLIIQADPPSTLEKFLGRIPMIENWVVSPPHYGQANVLGLPDTGGQIVYILD 301
 DB 254 ETHLLDLLEAEPPSTLEKFLGRIPMVFNVVNSPPHYGQANVLGLPDTGGQIVYILD 313
 QY 302 QVRALENEMVLRKXQGLDVSPKLIIVTRLIPDAKGTSCNQLERISQGTQRTYILRVFPR 361
 DB 314 QVRAMENEMLRKXQGLDNITPRILIVTRLIPDAKGTTCQRLKVLGTTEHTHLRVFPR 373
 QY 362 NENGILKXWISREDVWPYLETFAEDAAGEATAELQGTDFPIIGNYSDGNLVASLLSYKMG 421
 DB 374 TENGIVRKWISREFEVPYLETFTDDVAHEIAGELQANPDLTIGNYSDGNLVACLIHAKMG 433
 QY 422 ITQCNIAHALEKTKYPSDIFPKWDEKHYHFSQFTADIIAMNNADFLITSTYOEIAGSK 481
 DB 434 VTHCTIAHALEKTKYPSNDDLYWKFEDHYHFSQFTDIIAMNHADFLITSTYOEIAGNK 493
 QY 482 NTVGQYESHTAFTLPGLYRVVHGIDVDPKFNIVSPGADMSIYPPHTEKAKRLPSIHGSI 541
 DB 494 DTVGQYESHMAFTMPGLYRVVHGIDVDPKFNIVSPGADMSIYPPYSESRKRLTSLHPEI 553
 QY 542 ENLIYDPEQNDHGLHLDKSKPLTFESMARLDRVKNITGLVEAPAKAKLRELNVLVVA 601
 DB 554 EELLYSEVDNNEHFKMLKDRNKPIIFSMARLDRVKNITGLVELYGRNPRLOELNVLVVC 613
 QY 602 GYNDVANKSKDREIEIAETKMHSLIKTNLFGQPRWISAQTNRANGELXYIADTHGAFV 661
 DB 614 G-DHGNPSKDKESQAEFKKMFLLIEQVNLNGHFWISAQNNRVNGELYRYICTKGAFF 672
 QY 662 QPALYEAFGLTVVEAMTCGLPTFATLHGGPARIIEHGVSGPHIDPHYHPEQAVNLMAFPD 721
 DB 673 QPAFYEAFTLVESMTGCLPTATAYGSPAEIIVNGVSGPHIDPHYQGDKASALLVEFFE 732
 QY 722 RKQDDPHWNISSAGLORIYKWTWKIYSERLMTLAGVYGFVKYKSLERLETRRYLEM 781
 DB 733 KCQEDPSHWTKISQGGLORIEYKWTWKIYSERLMTLAGVYGFVKYKSVNLERRETRYLEM 792
 QY 782 FYILKFRFELAKTVPLAID 799
 DB 793 LYALKYRTMASTVPLAVE 810
 XX
 XX ADC08209 standard; protein; 816 AA.
 AC ADC08209;
 XX
 XX 18-DEC-2003 (first entry)
 XX Rice protein sequence Seq ID514 related to grain filling.
 XX
 XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 XX WO2003000905-A2.
 XX
 XX 03-JAN-2003.
 XX
 XX 21-JUN-2002; 2002WO-1B002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI

PI Glazebrook J, Katagiri F, Kreps J, Provart N, Rieke D;

XX WP2; 2003-229341/22.

DR N-PSDB; ADC08208.

XX New plant genes encoding polypeptides having an activity involved in or
PT associated with the synthesis, metabolism or degradation of carbohydrates
PT in the plant grain useful in generating plants having improved
PT nutritional properties.

PS Claim 34; SEQ ID NO 514; 130pp; English.

XX This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is the
CC amino acid sequence of a rice protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences.

XX Sequence 816 AA;

Query Match 70.5%; Score 2974; DB 7; Length 816;

Best Local Similarity 69.8%; Pred. No. 2e-261;

Matches 557; Conservative 105; Mismatches 134; Indels 2; Gaps 2;

QY 3 HASGRDVTTHAHRNELVALLSKYKNGKGLLOPHILDALDEVGSGR-ALASGPFJ 61
DB 14 HSRERIGDSLSAHNELVAVFTRLVNLGKMLQAHQIIAEYNNATSEADREKLKDGAFE 73
QY 62 DVLRSAQAIIVPPFAIVRPRPGVWEVVRNVNHELVSVEQLTVSEVLFKEELVQGN 121
DB 74 DVLRSAQGVIVSPVALAIRPRPGVWEVVRNVSELAVELLTVFYLQFKQLVEEGRN 133
QY 122 DPTVTELDPEPPNVSPVPRNRSSESGVQVQLNRLSSIMFRNRDCLBPLDPLRGRHK 181
DB 134 NNFWTELDPEPPNVSPVPRNRSSESGVQVQLNRLSSIMFRNRDCLBPLDPLRGRHK 193
QY 182 GHVMMNDRIQSLGSLQSVLTAEHLKSLPADTPYSQFAYKQEMKLEKGGDRAGHVL 241
DB 194 GMTMLNDRIRSLALQGLARXAEHLGSLSDTPYSEFHRFPQELGLEKGGDCAKRSQ 253
QY 242 EMIHLDDIIOAPDPSLEKFLGRIPMIENVVSPHGVFGQANVLGLPDTGQIVVILD 301
DB 254 ETIHLDDLEAPDPSLEKFLGTIPWVENVVIMSPHGVFAQANVLGYPDTGQIVVILD 313
QY 302 QVRALENMVLKXQGLDVSPKILIVTRILIPDAKGTSCNQLERISGTQHTYILRVPR 361
DB 314 QVRALENMVLKXQGLDVSPKILIVTRILIPDAKGTSCNQLERISGTQHTYILRVPR 373
QY 362 NENGILKXWISFDVWPYLETAEDAGSIAELQTPPTIGNYSYDGNLVSLLSYKNG 421
DB 374 TENGIVRWISFVWPYLETETDVAHIAELQANPOLIIGNYSYDGNLVSLLSYKNG 433
QY 422 ITQCNIAHALEKTKYPSDIPFKNFDEKHFSCQPTADIIAMNADPILITSTVQETAGSK 481
DB 434 VTHCTIAHALEKTKYPSDIPFKNFDEKHFSCQPTADIIAMNADPILITSTVQETAGSK 493
QY 492 NTVGQVESHATFLPGLYRVVHIGIDVDPKFNIVSPGADMSIYFPHTEKARLTSLSHGI 541
DB 494 DTWGQVESHATFLPGLYRVVHIGIDVDPKFNIVSPGADMSIYFPHTEKARLTSLSHGI 553
QY 542 ENLIYDPEQNEHGHLDHDKPILFMAARLVRNITGLVTEAPAKAKLRLNVLVVA 601
DB 554 EELLYSEVDNNEHFKMLKORNPILFMAARLVRNITGLVTEAPAKAKLRLNVLVVA 613

QY 602 GYNDVNSKORREIARIEKMHKILKTHLFGOPRWSAOTNRARNGELRYIADTHGAFV 661
DB 614 G-DHGNPSSKDEQAEFKKQFLLIQYNNLNGHIRWISAQNRVRNGELRYIADTHGAFV 672
QY 662 QPALYEAFLGTVVEAMTQGLPTPATLHGGPAETIEHGVSGFHIDPYHPEQAVNLMADFFD 721
DB 673 QPALYEAFLGTVVEAMTQGLPTPATLHGGPAETIEHGVSGFHIDPYHPEQAVNLMADFFD 732
QY 722 RCKQDDPHVNSGAGLQRIYKTYKTYSERLMTAGVYGFWKYVSKLRLRTRRYLEM 781
DB 733 KQEDPSHWTKISQGLQRIEYKTYKTYSERLMTAGVYGFWKYVSKLRLRTRRYLEM 792
QY 782 FYILKRELAKTVPLAID 799
DB 793 LYALKIRTWASIVPLAVE 810
RESULT 14
ADC68460
ID ADC68460 standard; protein; 815 AA.
XX ADC68460;
XX 18-DRC-2003 (first entry)
XX Lolium perenne fructan biosynthesis protein SEQ ID NO:170.
XX Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
XX biosynthetic pathway; plant.
XX Lolium perenne.
XX WO2003040306-A2.
XX 15-MAY-2003.
XX 07-NOV-2002; 2002WO-NZ000239.
XX 07-NOV-2001; 2001US-0337703P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIGHT-) WRIGHTSON SEEDS LTD.
XX Demmer J, Forster RL, Gibson JB, Shenk MA, Norriss MG, Glenn M;
XX Saulsbury KM, Hall C;
XX MPI; 2003-441544/41.
XX N-PSDB; ADC68424.
XX New polynucleotide encoding polypeptides from Lolium perenne or Festuca
XX arundinacea, useful for modulating the biosynthesis of lignin, fructan or
XX tannin in a plant.
XX Claim 18; SEQ ID NO 170; 240pp; English.
XX The present invention describes isolated polynucleotides (I) encoding
XX proteins (II) from Lolium perenne and Festuca arundinacea which are
XX active in lignin, fructan and tannin biosynthetic pathways. Also
XX described: (1) an isolated oligonucleotide probe or primer comprising at
XX least 10 contiguous residues complementary to 10 contiguous residues of
XX (I); (2) a kit comprising the oligonucleotide probe or primer; (3) a
XX genetic construct comprising (I); (4) a transgenic plant cell comprising
XX the genetic construct of (3); (5) a plant or its seed, fruit or progeny
XX comprising the transgenic plant cell of (4); (6) modulating one or more
XX of the lignin, fructan or tannin compositions of a plant; (7) producing a
XX plant having one or more of the lignin, fructan or tannin compositions;
XX and (8) modifying the activity of (II) involved in a lignin, fructan or
XX tannin biosynthetic pathway in a plant. (I) can be used for modulating
XX the biosynthesis of lignin, fructan or tannin in a plant. The present
XX sequence is used in the exemplification of the present invention.
XX Sequence 815 AA;
SQ

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 15:32:41 ; Search time 4542.4 seconds
(without alignments)
17993.23c Million cell updates/sec

Title: US-10-080-114A-1

Perfect score: 2737

Sequence: 1 gtcacccacgctccggcg.....aaaaaaagggcgccgc 2737

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2644.2	96.6	2705	11 AY104856	AY104856 Zea mays
2	1165.2	42.6	3056	13 BU103693	BU103693 SCCCR2100
3	1151	42.1	3140	11 AY103630	AY103630 Zea mays
4	794.6	29.0	1005	13 BQ619258	BQ619258 RNOSRQ5F0

5	793	29.0	938	13	BQ619406
6	722	26.4	835	14	CA280212
7	704.8	25.8	888	14	CB662799
8	702.8	25.7	909	14	CB629313
9	688.6	25.2	841	14	CB648550
10	684.6	25.0	886	14	CB628458
11	676.2	24.7	745	14	CD426853
12	676	24.7	836	14	CB631982
13	664	24.3	690	14	CD442316
14	655.6	24.0	808	14	CB651486
15	654.2	23.9	817	14	CB666247
16	647.6	23.7	797	14	CB647500
17	643.2	23.5	801	14	CB641607
18	637.2	23.3	727	13	CA066428
19	636.8	23.3	824	14	CB68706
20	636.8	23.3	860	14	CB627276
21	636.2	23.2	785	14	CB677314
22	634	23.2	802	14	CB633383
23	625.2	22.8	812	14	CB663333
24	623.6	22.8	807	14	CB633104
25	622	22.7	767	14	CB682789
26	620	22.7	804	14	CB627329
27	618.8	22.6	806	14	CB627200
28	615.8	22.5	836	14	CB635134
29	615.2	22.5	832	14	CB648734
30	613.6	22.4	839	14	CB645387
31	611.6	22.3	803	14	CB647961
32	610.6	22.3	833	14	CB631361
33	610.2	22.3	836	14	CB631302
34	607.8	22.2	779	14	CB635859
35	609.2	22.0	651	14	CP632182
36	599.2	21.9	800	14	CB628700
37	594	21.7	700	14	CA195492
38	593.2	21.7	787	14	CB629315
39	592.8	21.7	756	14	CB628904
40	580.6	21.2	763	14	CB673208
41	570.2	20.8	763	14	CB628938
42	560.6	20.5	727	14	CB632976
43	560	20.5	720	14	CA196779
44	545.4	19.9	628	14	CA283716
45	541.6	19.8	951	14	CF514627

ALIGNMENTS

RESULT 1
AY104856 2705 bp mRNA linear HTC 16-OCT-2002
LOCUS
DEFINITION Zea mays PC0079420 mRNA sequence.
ACCESSION AY104856
VERSION AY104856.1 GI:21207934
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 2705)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
AUTHORS Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.

TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of

Overgo Probes

JOURNAL Unpublished (2002)

REFERENCE 2 (bases 1 to 2705)

Coe,E.H.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

source
 .. 2705
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeDB:634420"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 96.6%; Score 2644.2; DB 11; Length 2705;
 Best Local Similarity 99.1%; Pred. No. 2.2e-311;
 Matches 2669; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

18 GCGACCGGTCGAGACACCCCTCCACGGCCACCGCAACGAGCTCGTGGCCCTCCTGTCCA 77
 |||||
 1 GCGACCGGTCGAGACACCCCTCCACGGCCACCGCAACGAGCTCGTGGCCCTCCTGTCCA 60
 |||||
 78 AGTACGTGAACAAGGGGAAGGCACTCTGACGCCGACCAATCTCGACGGCTCGAGC 137
 |||||
 61 AGTACGTGAACAAGGGGAAGGCACTCTGACGCCGACCAATCTCGACGGCTCGAGC 120
 |||||
 138 AGGTCCAGGGCTCCGGGGGCGGGCTAGCCGAGGGACCTTCTCGAGCTCCTCGCT 197
 |||||
 121 AGGTCCAGGGCTCCGGGGGCGGGCTAGCCGAGGGACCTTCTCGAGCTCCTCGCT 180
 |||||
 198 CGCGCCAGAGAGCGATCGTGTGCGCGCGTTCGTGGCCATCGCGTGGCCCGCGCGCG 257
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 181 CGCGCCAGAGAGCGATCGTGTGCGCGCGTTCGTGGCCATCGCGTGGCCCGCGCGCG 240
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 258 GAGTTGGAGTACGTCGCGCTCAACGTTCAAGCTCAGCTCAGCTCAGCTCAGCTC 317
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 318 CGAGTACCTCGCTTCAGAGAGAGCTTGTGAGCGCCAGCACATGATGATCCCTAGCTC 377
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 301 CGAGTACCTCGCTTCAGAGAGAGCTTGTGAGCGCCAGCACATGATGATCCCTAGCTC 360
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 378 TCGAGCTTGACTTCGAGCGCGTTCAGTGTCTCAGTCCACGCCCAATCGGTCACTCTA 437
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 361 TCGAGCTTGACTTCGAGCGCGTTCAGTGTCTCAGTCCACGCCCAATCGGTCACTCTA 420
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 438 TTGGAAACGGTGTGAGTCTCCCAACCGGACACTTGTCTCAATCATGTTCGCGCAACGG 497
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 421 TTGGAAACGGTGTGAGTCTCCCAACCGGACACTTGTCTCAATCATGTTCGCGCAACGG 480
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 498 ATTGCTTGGAGCCCTGTGTTGATTTCTCCGTCGCGCCACCGGACAGGGGCTATGATGA 557
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 558 TGCCTTAATGATAGATACAAAGCTTGGGGAGGCTTCAGTCTGTGTCGACCAAGCTGAGG 617
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www.zmdb.iastate.edu.
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1 (bases 1 to 1005)
AUTHORS
Wang, H. and Bohnert, H.J.
TITLE
Genomics of plant stress tolerance
JOURNAL
Unpublished (2002)
CONTACT
Mark Fredricksen
DEPARTMENT
Department of Plant Biology
UNIVERSITY
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
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  Genomics of plant stress tolerance
  Unpublished (2002)
  Contact: Mark Fredricksen
  Department of Plant Biology
  University of Illinois
  1201 W. Gregory Dr., Urbana, IL 61801, USA
  Tel: 2172655473
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  Contact: Arruda P
  Centro de Biologia Molecular e Engenharia Genetica
  Universidade Estadual de Campinas
  Caixa Postal 6010, 13083-970, Campinas SP, Brazil
  Tel: 55 19 3788 1137
  Fax: 55 19 3788 1089
  Email: parruda@unicamp.br
  Clone distribution: clone distribution information can be found
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growing in greenhouse; Vector: pSport1; Site 1: Sali;
Site 2: Not1; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CU-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucet.lad.ic.unicamp.br/public>

OR-GIN

Query Match 26.4%; Score 722; DB 14; Length 835;
Best Local Similarity 92.5%; Pred. No. 2.3e-78;
Matches 769; Conservative 0; Mismatches 62; Indels 1; Gaps 1;

QY 761 CGACGCCATCTACCTAGAGAAATCTTGGGAGAGATCCCATGATTTTAACTGTT 820
DB 1 CGACGCCATCAACCTTAGAGAAATCTTGGGAGAGATCCCATGATTTTAACTGTT 60
QY 821 GTGGTATCCCTCATGTGATCTTTGGTCAAGCTAAATGTTAGCTTGGCCAGACACAGGA 880
DB 61 GTGGTATCCCTCATGTGATCTTTGGTCAAGCTAAATGTTAGCTTGGCCAGACACAGGA 120
QY 881 GGCAGATCGTCTATATCTAGTCCCAAGTCCGCTGCTAGAAAATGAGATGTTCTCCGT 940
DB 121 GGCAGATCGTCTATATCTAGTCCCAAGTCCGCTGCTAGAAAATGAGATGTTCTCCGT 180
QY 941 TTAAGAAACAAGGCTTGATGTTTCCCAAGATTCATGTTTACTCGCTGATACCA 1000
DB 181 TTAAGAAACAAGGCTTGATGTTTCCCAAGATTCATGTTTACTCGCTGATACCA 240
QY 1001 GATGCAAAAGGACATCATCATCAGCGCTTGAGAGAAATGAGTGAACACACAGCATACT 1060
DB 241 GATGCAAAAGGACATCATCATCAGCGCTTGAGAGAAATGAGTGAACACACAGCATACT 300
QY 1061 TACATATTAAGAGTCCCTTCAGAAATGAAAAATGGGATCTTAAGAAATGGATATCAAGA 1120
DB 301 TACATATTAAGAGTCCCTTCAGAAATGAAAAATGGGATCTTAAGAAATGGATATCAAGA 360
QY 1121 TTTGATGTGGCCATCTGGAACATTTGCTGAGGATCTGCTGGTGAATGCTGCT 1180
DB 361 TTTGATGTGGCCATCTGGAACATTTGCTGAGGATCTGCTGGTGAATGCTGCT 420
QY 1181 GAATTACAGGTACTCCAGACTTCATAATTTGGAACCTACAGTGAATGAAATCTTGGCG 1240
DB 421 GAATTACAGGTACTCCAGACTTCATAATTTGGAACCTACAGTGAATGAAATCTTGGCG 480
QY 1241 TCATTGCTATCTTACAGATGGAAATTAACAGTGAACATTTGCTGATGCTCTGGAAAAG 1300
DB 481 TCATTGCTATCTTACAGATGGAAATTAACAGTGAACATTTGCTGATGCTCTGGAAAAG 540
QY 1301 ACTAAGTATCCAGATTCAGACATATTTGGAAGATTTGATGAGAGTACCATTTCTCC 1360
DB 541 ACTAAGTATCCAGATTCAGACATATTTGGAAGATTTGATGAGAGTACCATTTCTCC 600
QY 1361 TGGCAGTTCACTGCTGATATAATTTGCTATGAACAAATGCTGATTTATCATCACCAGCA 1420
DB 601 TGTGAGTCACTGCTGATATAATTTGCTATGAACAAATGCTGATTTATCATCACCAGCA 660
QY 1421 TACCAAGAAATTCG-TGGAAGCAAAATATCTGTTGGACAGTATGAGAGTCAATCTGCTT 1479
DB 661 TACCAAGAAATTCGTTGGAAGCAAAATATCTGTTGGACAGTATGAGAGTCAATCTGCTT 720
QY 1480 TACTCTGCTGCTGTGACGAGTGTGCTCCATGGATCGATGCTTTCATCCAAAGTTCAA 1539
DB 721 TACTCTGCTGCTGTGACGAGTGTGCTCCATGGATCGATGCTTTCATCCCTAAGATCA 780
QY 1540 TATAGTCTCTCTGGAGCTGACATGTCATATATCTTCCACATACCCAGAA 1590
DB 781 AATAAACCTCTTGAACCTTGAGGCTTCAATATATTTTCTTTTACCCCAA 831

RESULT 7
CB662799
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB662799 888 bp mRNA linear EST 09-APR-2003
OSJNEd07C12.f OSJNEd Oryza sativa (japocica cultivar-group) CDNA
clone OSJNEd07C12 5', mRNA sequence.
CB662799
CB662799.1 GI:29666524
EST.

Oryza sativa (japocica cultivar-group)

Oryza sativa (japocica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 888)

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,

Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: gta aaa cga cgg cca gtcg

BACKWARD: gga aac agc tat gac cat g

Plate: 07 row: C column: 12

Seq primer: gta aaa cga cgg cca gtcg.

Location/Qualifiers

1..888

/organism="Oryza sativa (japocica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="OSJNEd07C12"

/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEd"

/notes="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:

XhoI; 24 hrs after inoculation with Rice Blast (C924C-1)"

ORIGIN

Query Match 25.3%; Score 704.8; DB 14; Length 888;
Best Local Similarity 87.8%; Pred. No. 2.8e-76;
Matches 780; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

QY 691 GAAAGGTTGGGTGATACAGCAGACATGTTTGGAAATGATCCATCTCTCTAGACAT 750
DB 1 GAAGGTTGGGGCGACACAGCTGGATATGCTTGGAGATGATACATCTCTCTGGATG 60
QY 751 CATTCAGGCCCCAGACCCATCTACCCCTAGAGAAATCTTGGGAGGATCCCATGATTT 810
DB 61 GCTTCAAGCCCTGATCCATCTACTCTTGAGACGTTCTTGGGAAGGATCCCATGATCT 120
QY 811 TAACGTTGTTGGTATCCCTCATGATCTTGGTCAAGCTAATGATATAGCTTGCC 870
DB 121 TAATGTCGTGATGTCCTCATGATATTTGGCCAAAGCAATGTTGGGCTTACC 180
QY 871 AGACACAGGAGGACAGATCGTCTATATCTATCTGACCAAGTCCGTGCATAGAAATGAGAT 930
DB 181 AGATCTGAGGCGAGATGTCCTATATCTATCTGACCAAGTCCGTGCATGAGATGAGAT 240
QY 931 GGTTCCTCGTTTAAAGAAACAAGGCTTGATGTTTCCCAAGATTCATGTTACTCG 990
DB 241 GGTTCCTAGGTTAAAGAAACAAGGCTTGATGTTTACCCCTAAAATTTCTATTGTTACTCG 300
QY 991 GCTGATACAGATGCAAAAGGACATCATCATCAGCGCTTGAGAGATTAGTGAAC 1050

Db 301 GCTGATACCAGAGCAAGGACATCATGCAATCAGCGTCTTGAGAGTAAGTGGGAC 360
Qy 1051 ACAGCATACTTACATATTAAGAGTCCCTTCGAAATGAAATGSGTACTTAAAGAAATG 1110
Db 361 ACAACATACTTACATATTAAGAGTCCCTTCGAAATGAAATGSGTACTTAAAGAAATG 420
Qy 1111 GATATCAAGATTGATGTGGCCATATCTCGAAACATTTGCTGAGGATGCTGCTGCTGA 1170
Db 421 GATATCAAGATTGATGTGGCCATATCTCGAAACATTTGCTGAGGATGCTGCTGCTGA 480
Qy 1171 AATGCTGCTGAATTAAGGATCTTCCAGACTTCATAATTTGGAATGGAATGATGATGAA 1230
Db 481 GATTGCTGCAGAACTACAAAGGTACTCCAGACTTCATAATTTGGAATGGAATGATGATGAA 540
Qy 1231 TCTGTGCGCTGATGCTTATCTTACAGATGGAATTCACCGAGTGCACATGCTCATGCTC 1290
Db 541 TCTGTGCTGATGCTTATCTTACAGATGGAATTCACCGAGTGCACATGCTCATGCTC 600
Qy 1291 TCTGGAAGAACTAAGTATCCAGATTCAGACATATTTTGGAGAAATTTTGGATGAGAATTA 1350
Db 601 TTTGGAAAGAACTAATATCCAGACTCAGACATATCTTGGAGAAATTTTGGATGAGAATTA 660
Qy 1351 CCATTCTCTGCGGATGCTGCTGATATATTTGCTATGAAACAACTGATTTTATCAT 1410
Db 661 CCATTCTCTGCTGCTGCTGATATATTTGCTATGAAACAACTGATTTTATCAT 720
Qy 1411 CACGAGCATATCAAGAAATTTGCTGAGGAAATTTGCTGAGGAAATTTGCTGAGGAAATTT 1470
Db 721 CACGAGCATATCAAGAAATTTGCTGAGGAAATTTGCTGAGGAAATTTGCTGAGGAAATTT 780
Qy 1471 TACTGCTCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1529
Db 781 TACTGCTCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 1530 CAAGTTTCATATAGTCTCTCTGAGGCTGAGATGCTCATATATCTTC 1577
Db 841 CAAGTTTCATATAGTCTCTCTGAGGCTGAGATGCTCATATATCTTC 888

RESULT 8

CB629313

LOCUS

CB629313 OSIIIE05H07.f OSIIIEB Oryza sativa (indica cultivar-group) cDNA
clone OSIIIE05H07 5', mRNA sequence.

ACCESSION

CB629313

VERSION

CB629313.1 GI:29624302

KEYWORDS

Esr.

SOURCE

Oryza sativa (indica cultivar-group)

ORGANISM

Oryza sativa (indica cultivar-group)

REFERENCE

AUTHORS

Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,

Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe oryzae

Unpublished (2003)

Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,

Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

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between rice and Magnaporthe oryzae

Unpublished (2003)

Contact: Rod Wing

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85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 05 row: H column: 07

Seq primer: gta aac cga cgg cca gtc

Location/Qualifiers

source

1. .909

/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSIIIEB05H07"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIIEB"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"

ORIGIN

Query Match 25.7%; Score 702.8; DB 14; Length 909;
Best Local Similarity 86.9%; Pred. No. 4.8e-76;
Matches 773; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 402 ATGCTCAGTCCAGCCCAATCGTCAATCATATTCGCAACAGGATTTGCTTGGAGCCCTGCTGGATT 521
Db 19 ATGCTCAGTCCAGCCCAATCGTCAATCATATTCGCAACAGGATTTGCTTGGAGCCCTGCTGGATT 78
Qy 462 ACCGACATTTGCTCAATCATATTCGCAACAGGATTTGCTTGGAGCCCTGCTGGATT 521
Db 79 ACAGGCACTTTGCTTGGATCATATTCGCAACAGGATTTGCTTGGAGCCCTGCTGGATT 138
Qy 522 TCTTCGCTGGCCACCGGACAGGCGCATTTATGATGCTTAAATGATAGAAATCAAAAGCT 581
Db 139 TCTTCGCTGGCCACCGGATAGGGTCTATGATGCTTAAATGATAGAAATCAAAAGCT 198
Qy 582 TGGGAGGCTTTGAGTCTGCTGACCAAGCTGAGGAGCTTTGCAAGCTCCCTGCTG 641
Db 199 TGGGAGGCTTTGAGTCTGCTGACCAAGCTGAGGAGCTTTGCAAGCTCCCTGCTG 258
Qy 642 ACACACCATCTACCAATTTGCTTATAAATTTCAAGAGTGGGCGCTTGGAGAAAGGTTGG 701
Db 259 ACACACCATCTACCAATTTGCTTATAAATTTCAAGAGTGGGCGCTTGGAGAAAGGTTGG 318
Qy 702 GTGATACAGCAGGACATGTTTGGAAATGATCATCTCTTACAGATCATTCAGGCGC 761
Db 319 GCGACACAGTGGATATGCTTGGAGATGATACATCTCTTCTGGATGCTGCAAGCGC 378
Qy 762 CAGACCATCTACCTACAGAAATTTCTTGGGAGGATCCCATGATTTTAAAGTGTG 821
Db 379 CTGATCCATCTACCTTGGAGAGTCTTGGGAGGATCCCATGATTTTAAAGTGTG 438
Qy 822 TGGTATCCCTCATGATGATCTTGGTCAAGCTTAATGATGATGCTTGGAGACAGGAG 881
Db 439 TAGTGTCTCTCATGATGATTTTGGCCAAAGCAATGTTGGGCTTACCAGATCTGGAG 498
Qy 882 GACAGATGCTTATCTGACCAAGTCCGCTGACCTAGAAATGAGATGCTTCTCGTT 941
Db 499 GCGAGATGCTTATCTGACCAAGTCCGCTGACCTAGAAATGAGATGCTTCTCGTT 558
Qy 942 TAAAGAAACAGGCTGATGCTTCCCAAGATTTCTATTTACTCGCTGATACACAG 1001
Db 559 TAAAGAAACAGGCTGATGCTTCCCAAGATTTCTATTTACTCGCTGATACACAG 618
Qy 1002 ATGCAAAAGGAAACATGCAATCAGCGCTTGGAGAAATGATGGAACACAGCATCTT 1061
Db 619 AAGCAAAAGGAAACATGCAATCAGCGCTTGGAGAAATGATGGAACACAGCATCTT 678
Qy 1062 ACATATTACGAGTTCCTTCAAGATGGAATGGAATGGAATGGAATGGAATGGAAT 1121
Db 679 ACATATTACGAGTTCCTTCAAGATGGAATGGAATGGAATGGAATGGAATGGAAT 738
Qy 1122 TTGATGTGGCCATATCTGGAACATTTGCTGAGGATGCTGCTGCTGCTGCTGCTG 1181
Db 739 TTGATGTATGCGCTTACCTGGAGAAATTTGAGAGGATGCTGCTGCTGCTGCTG 798
Qy 1182 AATTCAAGGCTTCTCAGACTTCATAATTTGAAACTACAGTGAATGGAATCTTGTGGCT 1241
Db 799 AACTTCAAGGCTTCTCAGACTTCATAATTTGAAACTACAGTGAATGGAATCTTGTGGCT 858

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QY 1242 CATTGCTATCTTACAGATGGGATTTACCAGTGCAGACATTTGCTCATGCT 1291
Db |||||||
859 CATTGCTATCTTACAGATGGGATTTACCAGTGCAGACATTTGCTCATGCT 908

RESULT 9
CB648550
LOCUS OSJNEB11P18.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEB11P18 5', mRNA sequence.
ACCESSION CB648550
VERSION CB648550.1 GI:29643543
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 841)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: P column: 18
Seq primer: gta aaa cga cgg cca gtc.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEB11P18"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
/clone_lib="OSJNEB"
/notes="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (Che
86061)"

ORIGIN
Query Match 25.2%; Score 688.6; DB 14; Length 841;
Best Local Similarity 88.8%; Pred. No. 2.6e-74;
Matches 745; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 923 AATGAGATGTTCTTCCTTTAAGAAACAAAGCGCTTGATTTCCCAAGATTTCTCAT 982
Db |||||||
2 AATGAGATGTTCTTAGTTTAAAGAAACAAAGCGCTTGATTTTACCCCTAAAATCTTTATT 61

QY 983 GTTACTCGGCTGATACCAGATGCAAAAGGAACATCATGCAATCAGCGCTTGAGAGAATT 1042
Db |||||||
62 GTTACTCGGCTGATACCAGAAAGCAAGCAAGGGAATCATCATGCAATCAGCGCTTGAGAGAATA 121

QY 1043 AGTGGAAACACAGCATCTTACATATTACAGTTCCCTTCAGAAATGAAATGGGATCTT 1102
Db |||||||
122 AGTGGAAACACACATCTTACATATTACAGTTGCCATTCAGAGTGCATTCAGAAATGAAATGGGATCTC 181

QY 1103 AAGAAATGGATATCAAGATTTGATGTGTGGCCATATCTGGAAACATTTGCTGAGGATGCT 1162
Db |||||||
182 AGGAAATGGATATCAAGATTTGATGTGTGGCCCTTACCTGGGAAATTTGCGAGGATGCT 241

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QY 1163 GCTGGTGAATTTGCTGCTGAATTTCAAGGTACTTCCAGACTTTCATATTTGGAAACTACGT 1222
Db |||||||
242 GCTGGTGAATTTGCTGCTGAATTTCAAGGTACTTCCAGACTTTCATATTTGGAAACTACGT 301

QY 1223 GATGAAATCTTTGTGGCGTCAATGCTATCTTCAAGATGGGAATACCCAGTGCACATT 1282
Db |||||||
302 GACGGTAATCTTTGTTCATCAATGCTATCTTCAAGATGGGAATACCCAGTGCACATT 361

QY 1283 GCTCATGCTCTGGAAAGACTAAGTATCCAGATTCAGACATATTTTGGAGAAATTTTCGAT 1342
Db |||||||
362 GCTCATGCTCTGGAAAGACTAAGTATCCAGATTCAGACATATTCAGTGGAGCAAGTAGCAT 421

QY 1343 GAGAATACCAATTTCTCTGCCAGATTCACCTGCTGATATATTTGCTATGAACAATGCTGAT 1402
Db |||||||
422 GAGAATACCAATTTCTCTGCTGATATATTTGCTGATATATTTGCTGATATATTTGCTGAT 481

QY 1403 TTTATCATCACAGACATATCACCAAGAAATTTGCTGGAGCAAAATATCTTTGACAGATAT 1462
Db |||||||
482 TTTATTAATCACAGACATATCACCAAGAAATTTGCTGGAGCAAAATATCTTTGACAGATAT 541

QY 1463 GAGAGTCATACCTGCTTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1522
Db |||||||
542 GAGAGTCATACCTGCTTTACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601

QY 1523 TTCGATCCAAAGTTCAATATATAGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
Db |||||||
602 TTTGACCCAAAGTTCAATATATAGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661

QY 1583 ACCGAGAGCCCAAGCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1642
Db |||||||
662 ACTGAAAGCCCAAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 721

QY 1643 CCGGAGCAAAACGATGAACAATTTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1702
Db |||||||
722 CCAGAGCAAAATGACGAAATATTTGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 781

QY 1703 TCCATGCGAAGACTCGACAGCGTGAAGAAACATTAACAGGGCTGCTGCGAAGCTTTTGCTAA 1761
Db |||||||
782 TCCATGCGAAGACTTGACCGAGTTAAGAAACATTAACAGGGCTGCTGCGAAGCTTTTGCTAA 840

RESULT 10
CB628458 886 bp mRNA linear EST 08-APR-2003
LOCUS OSJIEB04A18.f OSJIEB Oryza sativa (indica cultivar-group) cDNA
DEFINITION clone OSJIEB04A18 5', mRNA sequence.
ACCESSION CB628458
VERSION CB628458.1 GI:29623447
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 886)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
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Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: A column: 18
Seq primer: gta aaa cga cgg cca gtc.

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FEATURES	source	Location/Qualifiers
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	/tissue_type="Leaf"	
	/dev_stage="3 week"	
	/lab_host="DH10B"	
	/clone_lib="OSIIEB"	
	/notes="vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"	
ORIGIN		
Query Match	25.0%;	Score 684.6; DB 14; Length 886;
Best Local Similarity	86.5%;	Pred. No. 7.7e-74;
Matches 767;	Conservative 0;	Mismatches 119; Indels 1; Gaps 1;
Qy	178	CTTCTCGAGTCTCTCCGCTCCGCGCAGGAGCGATCGTGTGCGCGCTGTCGCGCAT 237
Db	1	CTTCTCGAGTCTCTCCGCTCCGCGCAGGAGCGATCGTGTGCGCGCTGTCGCGCAT 60
Qy	238	CGCGTGGCGCGCGCGCGGAGTTTCGGAGTAGCTCCGGGTCAAGTTCACGAGCTCAG 237
Db	61	CGCGTGGCGCGCGCGCGGAGTTTCGGAGTAGCTCCGGGTCAAGTTCACGAGCTCAG 120
Qy	298	CGTCGAGCAGCTCACAGTCTCGGAGTAGCTCCGCTTCAAGGAGGAGCTTGTGCAGCGCCA 357
Db	121	CGTCGAGCAGCTCACAGTCTCGGAGTAGCTCCGCTTCAAGGAGGAGCTTGTGCAGCGCCA 180
Qy	358	GCACAAATGATCCCTACGCTTTCGAGCTTGAGCTTCGAGCGGTCAATGCTCAGTCCCACG 417
Db	181	GTCACAGATCCGTTACATCTTGGAGCTTGAATTTGAGGAGTCAATGAGTCCGTTCCAG 240
Qy	418	CCCAATTCGGTCAATCTATTGGAACGGTGTGAGTTCCTCAACGAGTTCAGTTCGCTC 477
Db	241	CCCAATTCGGTCAATCTATTGGAACGGTGTGAGTTCCTCAACGAGTTCAGTTCGCTC 300
Qy	478	AATCAGTTCGCGCAACGAGGATTCCTTGGAGCGCCCTGTTGGATTCTCTCGTGGCCACG 537
Db	301	GATCAGTTCGCGCAACGAGGATTCCTTGGAGCGCCCTGTTGGATTCTCTCGTGGCCACG 360
Qy	538	GCACAGGGGCATGTTATGATGCTTAAATGATGAATAAAAGCTTGGGAGGCTTCAGTC 597
Db	361	GCATAAGGTCATGTCATGATGCTAAATGACAGATACAGAGTCTGGAGAGCTTCAGTC 420
Qy	598	TGTGCTGACCAAGCTGAGGAGCACTTGTCAAGCTCCCTGTGTGACACCACTACTCACA 657
Db	421	TGTGCTGACCAAGCTGAGGAGCACTTGTCAAGCTCCCTGTGTGACACCACTACTCACA 480
Qy	658	ATTGTGCTTATAAATTCAAGAGTGGGCGCTGGAGAAAGTTGGGGTGTATACACGAGCA 717
Db	481	GTTCCGCAATTAAGTTTCAAGATGGGANTTGGAGAGGGTTGGGGGACACAGCTGGATA 540
Qy	718	TGTTTTGGAAATGATCCATCTCCTTCAGACATCATTCAGCGCGCCAGCCCATCTACCT 777
Db	541	TGCTTGGAGATGATACATCTCCTTCGGATGTGCTCAAGCGCCTGATCCATCTACTCT 600
Qy	778	AGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTTGTGTGAGTATCCCTCATGG 837
Db	601	TGAGACGCTTCTTGGGAAGGATCCCATGATTTTAAAGTTGTGTGAGTATCCCTCATGG 660
Qy	838	ATCTTTGTCACAGCTAATCTATTAGGCTTGGCAGACACAGGAGGACAGATCTCTATAT 897
Db	661	ATATTTGGCCAGCCAAATGTGTTGGGCTTACCAGATACTGGAGGGCAGATTTCTCTATAT 720
Qy	898	ACTGGACCAAGTCCGTGCATCAGAAATGAGATGTTTCCGTTTAAAGAAACAAAGGCT 957
Db	721	ACTGGACCAAGTCCGTGCATCAGAGATGAGATGTTTCTTAGTTTAAAGAAACAAAGCCT 780
Qy	958	TGATGTTTCCCCAAGATTCCTATTGTTACTCGGCTGATACAGATGTCAAAGGAAATC 1017

710 GCAGACATGTTTGGAAATGATCCATCTCCTTCTAGACATCAATTCAGCGCCACACCA 769
 Db GCAGACATGTTTGGAAATGATCCATCTCCTTCTAGACATCAATTCAGCGCCACACCA 120
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 Db CCTCATGATATCTTGGTCAAGCTAATGATTTAGGCTTGCAGACACACAGGACAGAT 240
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 950 CAGGGCTTGTATTTCCCAAGATTTCTCATGTTTACTCGGCTGATACAGATCCAAA 1009
 Db CAGGGCTTGTATTTCCCAAGATTTCTCATGTTTACTCGGCTGATACAGATCCAAA 360
 1010 GGAACATCATCAATCAGCGGCTCAGAGAAATAGTGGAAACACAGCATATCTTACATATTA 1069
 Db GGAACATCATCAATCAGCGGCTCAGAGAAATAGTGGAAACACAGCATATCTTACATATTA 420
 1070 CGAGTTCCCTTCAGAAATGAAATGGATCTTAAAGATGATATCAAGATTTGATG 1129
 Db CGAGTTCCCTTCAGAGATGAAATGGATCTTAAAGATGATATCAAGATTTGATG 480
 1130 TGGCCATCTCGAAACATTTCTGAGGATGCTGCTGTTGATGATCTGCTGAATACAA 1189
 Db TGGCCATCTCGAAACATTTCTGAGGATGCTGCTGTTGATGATCTGCTGAATACAA 540
 1190 GTTACTCCAGATCTCATATTTGAAACTACAGTATGATGGAAATCTTCTGGGCTCATTTGCTA 1249
 Db GTTACTCCAGATCTCATATTTGAAACTACAGTATGATGGAAATCTTCTGGGCTCATTTGCTA 600
 1250 TCTTACAGATGGAAATACCCAGTCCAAATTCATGCTCATGCTCGAAAGATCAATAT 1309
 Db TCTTACAGATGGAAATACCCAGTCCAAATTTGCTCATGCTCGAAAGATCAATAT 660
 1310 CAGATTGACATAT-TTGGAGATTTTCGATGAGAGTACATTTCT-CCTGGCCAGT 1367
 Db CAGATTGACATAT-TTGGAGATTTTCGATGAGAGTTCGATGAGAAATATCATTTCTCCCTGTGCT 720
 1368 TCATCTGCTGATATTAATTTGCTATCAA 1392
 Db TCATCTGCTGATATTAATTTGCTATCAA 745

RESULT 12
 CB631982
 LOCUS CB631982
 DEFINITION OS11EB09015.f OS11EB Oryza sativa (indica cultivar-group) cDNA
 clone OS11EB09015 5', mRNA sequence.
 ACCESSION CB631982
 VERSION CB631982.1 GI:29626971
 KEYWORDS EST.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 836)
 Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
 Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
 Large-scale identification of ESTs involved in the interaction
 between rice and Magnaporthe grisea
 Unpublished (2003)
 CONTACT: Rod Wing
 ARIZONA GENOMICS INSTITUTE
 UNIVERSITY OF ARIZONA
 BIOLOGICAL SCIENCES WEST, 448A, P.O. BOX 210088, TUCSON, AZ
 85721-0088, USA

Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: gta aaa cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
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 Seg primer: gta aaa cga cgg cca gtcg.
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 Best local Similarity 88.0%; Pred. No. 8.7e-73;
 Matches 736; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
 QY 641 GACACACCATCTACACAAATTTGCTTATAAATTTCAAGAGTGGGGCTGGAGAAAGGTTGG 700
 Db 1 GACACACCATCTACACAAATTTGCTTATAAATTTCAAGAGTGGGGCTGGAGAAAGGTTGG 60
 QY 701 GGTGATACAGCAGGACATGTTTGGAAATGTCATCTCCTCTAGACATCATTCAGCGG 760
 Db 61 GGGACACACGCTGGATATGTCCTGGAGATGATACATCTCCTCTGGATGCTGCAAGCG 120
 QY 761 CCAGACCCATCTACCTAGAGAAATTTCTGGGAGAGTCCCATGATTTTAAAGTGT 820
 Db 121 CCGTATCCATCTACTCTTGGAGAGTCTTGGGAGAGTCCCATGATTTTAAAGTGT 180
 QY 821 GTGSTATCCCTCATGGATCTTTGGTCAAGCTTAATGATTTAGGCTTGGCAGACACAGGA 880
 Db 181 GTAGTGTCTCTCATGGATATTTGGCCAAAGCAATGTTGTGGCTTTACAGATACCTGA 240
 QY 881 GGAAGATCCCTCATGGATCTTTGGTCAAGCTTAATGATTTAGGCTTGGCAGACACAGGA 940
 Db 241 GGGCAGATTTGCTATATATCTGGA CCAAGTCCGTCATTTGGAGATGAGATGTTCTTAGG 300
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Db      661 ACTAATATCCAGACTCAGACATATACCTGGACGAAGTAOGATGAGAAGTACCATTTCTCC 720
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Db      721 TGTCACTTCCAGCTGATTAATTCGCGCATGAACAAATGCTGATTTTATATATCACCAGCACA 780
QY      1421 TACCAAGAAATGCTGCGAAGCAAAATATCTGTTGGACAGATGAGAGTCTATCTGC 1476
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RESULT 13
CD442316 690 bp mRNA linear EST 03-JUN-2003
LOCUS EL01NC407H07.b Endosperm_4 Zea mays cDNA, mRNA sequence.
DEFINITION CD442316
ACCESSION CD442316.1 GI:31357959
VERSION 1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 690);
Author(s) Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
Sequencing of the maize endosperm ESTs
Unpublished (2002).
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.

FEATURES
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XhoI"

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Best Local Similarity 97.8%; Pred. No. 2.7e-71;
Matches 673; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      898 ACTGGACCAAGTCCTGCTGACTAGAAATGAGTGGTTCTCGTTTAAAGAAACAAGGGCT 957
Db      3 ACAGGCGCAAGGGCGTGCCTAGAAAATGAGTGGTTCTCGTTTAAAGAAACAAGGGCT 62

QY      958 TGAATGTTCCCAAGATCTCTATCTGTTACCTCGGCTGATACCAAGTCCAAAGGACATC 1017
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QY      1018 ATGCAATCAGCGGCTTGAGAGAATTAGTGGAAACACAGCATACTTACATATTACGAGTTCC 1077
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QY      1078 CTTTCAGAAATGAAATGGGATCTTAAAGAAATGGATATCAAGATTGATGTGGCCATA 1137
Db      183 CTTTCAGAAATGAAATGGGATCTTAAAGAAATGGATATCAAGATTGATGTGGCCATA 242

QY      1138 TCTGGAAACATTTGCTGAGCATCTCTGCTGGAATTTGCTGCTCAATTCAGAGTACTCC 1197
Db      243 TCTGGAAACATTTGCTGAGCATCTCTGCTGGAATTTGCTGCTCAATTCAGAGTACTCC 302

QY      1198 AGACTTCATAATTGGAACTACAGTATGATGGAATCTTTGTGGCGTCACTTGCTATCTTACAA 1257

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Db      303 AGACTTCATATTTGAAACTTACAGTGTGAAATCTTGTGGCATCGTTGCTATCTTACAA 362
QY      1258 GATGGGAATTCACAGTGCACATTTGCTCATGTCTCGAAAGAAAGTAAAGTATCAGATTC 1317
Db      363 GATGGGAATTCACAGTGCACATTTGCTCATGTCTCGAAAGAAAGTAAATATCAGATTC 422
QY      1318 AGACATATTTTGAAGAATTTGCTGATGAGAGTACCAATTTCTCTGCCAGTTCACGCTGA 1377
Db      423 AGACATATTTTGAAGAATTTGCTGATGAGAGTACCAATTTCTCTGTCAGTTCACGCTGA 482
QY      1378 TATAATTTCTATGAACAAATGCTGATTTTATCATCACCAGCACATACCAAGAAATTTGCTGG 1437
Db      483 TATAATTTGCTATGAACAAATGCTGATTTTATCATCACCAGCACATACCAAGAAATTTGCTGG 542
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Db      543 AAGCAAAATATCTGTTGGACAGATGAGAGTATCATCTGCTTTACTTGCCTGCTGCTGTA 602
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RESULT 14
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LOCUS OSJNEB16H11.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEB16H11 5', mRNA sequence.
ACCESSION CB651486
VERSION 1
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 808)
Author(s) Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 488A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gta g
BACKWARD: gga aac agc tat gac cat g
Plate: 16 row: H column: 11
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Best Local Similarity 88.3%; Pred. No. 2.6e-70;
Matches 712; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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DB 2 TTTCAAGATGGGGCTTGGAGAGGGTGGGGCGACACAGCTGGTATGCTTGGAGTG 61

QY 731 ATCCATCTCTTTAGACATCATTTAGGCGCCAGACCCCATCTACCTAGAGAAATTTCTTG 790
DB 62 ATACATCTCTTTCTGGATGCTTCAAGCGCTGATCCATCTACTCTTGGAGAGCTTCTTG 121

QY 791 GGGAGATCCCCATGATTTTAAAGTGTGTGGTATCCCTCATCGGATACTTTGGTCAA 850
DB 122 GGAAGGATCCCCATGATCTTTAATGTCTGTAGTGTCTCTCATGGATATTTTGGCCAA 181

QY 851 GCTAATGTATTAGGCTTGCACACAGCAGGACAGATCGTCTATATCTGACCAAGTC 910
DB 182 GCCAATGTGTGGCTTACCAGATCTGAGGCGGAGATGCTATATCTATCTGACCAAGTC 241

QY 911 CTTGCACTAGAAATGAGATGTTCTCCGTTTAAAGAAACAAGGCTTGCATGTTCCCA 970
DB 242 CTTGCAATGGAGATGAGATGTTCTTAGGTTAAAGAAACAAGGCTTGCATTTACCCCT 301

QY 971 AAGATCTCATTTACTCGGCTGATACAGATGCAAGAGGACATCATGCAATCAGCG 1030
DB 302 AAAATCTTATTTACTCGGCTGATACAGAGCAAGAAAGGACATCATGCAATCAGCGT 361

QY 1031 CTTGAGAGATTTAGTGGAAACACAGCATCTTACATATTACGAGTTCCTTTAGAAATGAA 1090
DB 362 CTTGAGAGATTTAGTGGGACACACATCTTACATATTACGAGTTCCTTTAGAAATGAA 421

QY 1091 AATGGATCTTTAAGAAATGAGATCAAGATTTGATGTGTGGCCATATCTGAAACATTT 1150
DB 422 AATGGATCTTACGAAATGAGATCAAGATTTGATGTGTGGCCATATCTGAAACATTT 481

QY 1151 GCTGAGGATGCTGCTGGTGAATTCGCTGATTAAGATTAAGGATTAAGGATTAAGT 1210
DB 482 GCGAGGATGCTGCTGGTGGAGATTCGTCAGAACTACAAAGTACTTCCAGATTCATTAAT 541

QY 1211 GGAACTACAGTGGTGGAAATCTTTGGGCTCATTCCTATCTTACAAGATGGAAATACC 1270
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QY 1271 CAGTGGCAATTTGCTCATGCTCTGAAAGAGATTAAGTATCCAGATTCAGACATATTTGG 1330
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QY 1331 AAGAAATTTGNTGAGAGTACCATTTCTCTCCAGTTCACCTGCTGATATATTTGCTATG 1390
DB 662 ACGAGTACGATGAGAGTACCATTTCTCTCTGAGTTCACAGCTGATATATTTGCGCATG 721

QY 1391 AACATGCTGATTTTATCATCACAGCATATCCAGAAATTTGCTGGAAGCAAAATATCT 1450
DB 722 AACATGCTGATTTTATATATCACAGCATATCCAGAAATTTGCTGCGAGCAAAACACA 781

QY 1451 GTTGACAGTATGAGGTCAATCTGC 1476
DB 782 GTTGACAGTATGAGGCCATCTGC 807

RESULT 15
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LOCUS
DEFINITION
CB666247.1 OSJUNED13B05 5', mRNA sequence.
ACCESSION
CB666247.1
VERSION
CB666247.1
KEYWORDS
EST.
ORyza sativa (japonica cultivar-group)

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ORyza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 817)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat sac cat g
Plate: 13 row: B column: 05
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 3.8e-70;
Matches 724; Conservative 0; Mismatches 93; Indels 4; Gaps 1;

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QY 1060 TTACATATTACGATTCCTTCAGAAATGAAATGGATCTTAAGAAATGGATATCAAG 1119
DB 61 TTACATATTACGATTCCTTCAGAAATGAAATGGATCTTAAGAAATGGATATCAAG 120

QY 1120 ATTTGATGTGGCCATATCTGAAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGC 1179
DB 121 ATTTGATGTGGCCATCTACCTGAGAAATTTGACAGAGATGCTGCTGGTGGATTTGCTGC 180

QY 1180 TGAATTAAGGTACTTCCAGATTCATTAATTTGAAACTACAGTATGGAATTTGCTGC 1239
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QY 1240 GTCAATGCTATCTTCAAGATGGAATTTACCCAGTGCACATTTGCTCATGCTCTGGAATA 1299
DB 241 ATCAATGCTATCTTCAAGATGGAATTTACCCAGTGCACATTTGCTCATGCTCTGGAATA 300

QY 1300 GACTAAGTATCCAGATTCAGACATATTTTGGAAATTTTCGATGAGAAGTACCAATTTCTC 1359
DB 301 GACTAATATCCAGATTCAGACATATCTGAGAGTACGATGAGAAGTACCAATTTCTC 360

QY 1360 CTGCCAGTTCACTGCTGATATTAATTTGCTATGAAATGCTGATTTTATCATCACAGCAC 1419
DB 361 CTGTCAGTTTCACTGCTGATATTAATTTGCTATGAAATGCTGATTTTATCATCACAGCAC 420

QY 1420 ATACCAGAAATTTGCTGGAAGCAAAATACTCTGTCAGATGATGAGAGTCACTGCTCT 1479
DB 421 ATACCAGAAATTTGCTGGAAGCAAAATACTCTGTCAGATGATGAGAGTCACTGCTCT 476

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 14:41:46 ; Search time 7059.61 Seconds
(without alignments)
16926.829 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

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Gapop 10.0 , Gapext 1.3

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Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	1888	68.5	2763	8	AK102158 Oryza sat
5	1809.6	65.6	2412	6	AX653034 Sequence
6	1353.4	49.1	2765	8	AB022091 Citrus un
7	1352.2	49.0	2848	8	AB001071 Pisum sat
8	1316	47.7	2787	8	AB045710 Pyrus pyr
9	1264.8	45.9	2679	8	AY205302 Solanum t
10	1262.8	45.9	2648	8	CPL132000 Craterost
11	1249.8	45.3	2430	6	AX507720 Sequence
12	1249.8	45.3	2506	8	AY142511 Arabidops
13	1249.8	45.3	2898	8	AY056784 Arabidops
14	1249.8	45.3	2904	8	AY051001 Arabidops
15	1179.6	42.8	2706	8	CPL131999 Craterost
16	1177.8	42.7	2563	6	A41498 Sequence 4
17	1177.8	42.7	2563	6	AR032247 Sequence
18	1177.8	42.7	2563	8	X81974 B.vulgaris
19	1173.4	42.6	2908	8	BVSSMRNA
20	1170	42.4	2910	8	MZBSUSIA
21	1162.6	42.2	2890	8	AF412037 Bambusa o
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24	1162.6	42.1	2451	6	AX755420 Sequence
25	1162.6	42.1	2451	6	AX755773 Sequence
26	1155.6	41.9	2652	8	AK100334 Oryza sat
27	1142.6	41.4	2842	8	AF030231 Glycine m
28	1133.6	41.1	2676	8	TASUCSYN1
29	1133	41.1	2494	6	E55472
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31	1133	41.1	2702	8	AK098923
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33	1133	41.1	3389	8	AK100546 Oryza sat
34	1132.6	41.1	2906	6	BD236049 Materials
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ALIGNMENTS

RESULT 1
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DEFINITION Zea mays sucrose synthase mRNA, partial cds.
ACCESSION AY059416
VERSION AY059416.1 GI:16797784
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2710)
Carlson,S.J.; Chourey,P.-S.; Helentjaris,T. and Datta,R.
REFERENCE
AUTHORS Gene expression studies on developing kernels of maize sucrose
TITLE

Pred. No. is the number of results predicted by chance to have a

synthase (SuSy) mutants show evidence for a third SuSy gene
Plant Mol. Biol. (2001) In press
2 (bases 1 to 2710)
JOURNAL
REFERENCE
AUTHORS Helentjaris, T.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2001) Agronomic Traits/TeTD, Pioneer Hi-Bred,
7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA
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ORIGIN

Query Match 98.1%; Score 2703.6; DB 8; Length 2710;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2706; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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RESULT 2
AY124703
LOCUS
DEFINITION
Zea mays sucrose synthase 3 mRNA, complete cds.
ACCESSION
AY124703
VERSION
AY124703.1
KEYWORDS
GI:22121989
SOURCE
Zea mays
ORGANISM
Zea mays
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REFERENCE
1 (bases 1 to 2837)
Holtgraewe,D.L., Scholz,A., Altmann,B. and Winter,H.
Complete coding sequence of a third sucrose synthase isoform in maize
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2837)
Holtgraewe,D.L., Scholz,A., Altmann,B. and Winter,H.
Direct Submission
TITLE
Submitted (20-JUN-2002) Biology, University of Osnabrueck, Barbara Straese 11, Osnabrueck 49076, Germany
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Location/Qualifiers
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ORIGIN
Query Match 88.3%; Score 2435.6; DB 8; Length 2837;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2581; Conservative 0; Mismatches 14; Indels 127; Gaps 1;
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 Oryza sativa (japonica cultivar-group) cDNA clone:J033086F24, full
 insert sequence.

AK102158
 AK102158.1 GI:3287367
 FLI CDNA; CAP trapper.

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1

The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team,
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group: Ootomo, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurokawa, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Aizawa, T., Itoh, M.,
 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
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 Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice

Science 301 (5631), 376-379 (2003)
 2752273
 12869764

2 (bases 1 to 2763)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
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 Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
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 Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
 Yoshimura, A.

Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
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 305-8602, Japan (E-mail: shikuchi@nias.affrc.go.jp,
 Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica
 rice.
 URL : http://cdna01.dna.affrc.go.jp/cdna/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
 Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
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 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center
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 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
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 Yasunishi, A. and Hayashizaki, Y.

Location/Qualifiers
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ORIGIN

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 Matches 2092; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

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Ehrhartoideae; Oryzeae; Oryza.
1

Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Qu, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
 Plant genes involved in defense against pathogens
 Patent: WO 03000898-A 2904 03-JAN-2003;
 Syngenta Participations AG (CH)

FEATURES
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RESULT 6

AB022091
LOCUS Citrus unshiu CitsUSA 2765 bp mRNA linear PLN 25-JAN-2002

DEFINITION Citrus unshiu CitsUSA mRNA for sucrose synthase, complete cds.

ACCESSION AB022091

VERSION AB022091.1 GI:6682840

KEYWORDS sucrose synthase.

SOURCE Citrus unshiu

ORGANISM Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE 1
Komatsu, A., Moriguchi, T., Koyama, K., Omura, M. and Akihama, T.
Analysis of sucrose synthase genes in citrus suggests different
roles and phylogenetic relationships
J. Exp. Bot. 53 (366), 61-71 (2002)

JOURNAL MEDLINE 21606208

PUBMED 11741042

REFERENCE 2 (bases 1 to 2765)
Komatsu, A.
Direct Submission
Submitted (22-DEC-1998) Akira Komatsu, National Institute of Crop
Science, 2-1-18, Tsukuba Science City, Ibaraki 305-8518, Japan
(E-mail: akomatsu@affrc.go.jp, Tel: 81-298-38-8949,
Fax: 81-298-38-8949)

FEATURES
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ORIGIN

Query Match 49.1%; Score 1353.4; DB 8; Length 2765;
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 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
 Pisum.
 REFERENCE 1
 AUTHORS Buchner, P., Poret, M. and Rochat, C.
 TITLE Cloning and Characterization of a cDNA (Accession No. AJ001071).
 JOURNAL Encoding a Second Sucrose Synthase Gene in Pea (Pisum sativum L.)
 REFERENCE 2
 JOURNAL Plant Physiol. 117, 719-719 (1998)
 AUTHORS Buchner, P.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-1997) Buchner P., Metabolisme, INRA-Versailles,
 Route de St. Cyr, Versailles-cesdex, 78026, FRANCE
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 AUTHORS Buchner, P.
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Route de St. Cyr, Versailles-cedex, 78026, FRANCE
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3'UTR

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ORIGIN

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Best Local Similarity 72.9%; Pred. No. 9.3e-217;
Matches 1757; Conservative 0; Mismatches 648; Indels 6; Gaps 1;
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RESULT 8
AB045710
LOCUS
DEFINITION
AB045710
ACCESSION
VERSION
AB045710.1
KEYWORDS
SOURCE
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ORGANISM
Pyrus pyrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
REFERENCE
1

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AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Tanase, K., Shiratake, K., Mori, H. and Yamaki, S.
Changes in the phosphorylation state of sucrose synthase during
development of Japanese pear fruit
Physiol. Plantarum 114 (1), 21-26 (2002)
11982930
2 (bases 1 to 2787)
Tanase, K., Yamaki, S. and Mori, H.
Direct Submission
Submitted (06-JUL-2000) Koji Tanase, Nagoya University, Graduate
School of Bioagricultural Sciences; Chikusa, Nagoya, Aichi
464-8601, Japan (E-mail: i000043r@box.media.nagoya-u.ac.jp,
Tel: 81-52-789-4028, Fax: 81-52-789-4025)
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Qy 303 CGTTCAGGCTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACCTCGGCTTCAAGGAGGA 362
Db 405 TGTATATGAGCTAAGTGTGAGGAAATTGACCGTTTCTGAATATCTTCACTTTAAGAAGA 464

ORIGIN

QY	363	GCTTGTGACGGCCAGACCAATGATGCCCTCTGAGCTTGACCTTGAGACCGGTCAA	422
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QY	423	TGTCCTCAGTCCACGCGCCAAATCGTGTCACTCATCTATTGSAACCGGTGTCAGTTTCTCCAA	482
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QY	483	CCGACACTTGTCTCAATCATCTGTTCCGCAAACAGGGATTCCTTGAGAGCCCTGTTGGATTT	542
Db	585	CGGCACCTTCTTCAATTATGTTCCGTAAACAGAGAACTGTTGGATCCATTACTTGATTT	644
QY	543	CTCTCGTGGCCACCGGCACAGGGCGATGTTATGATGCTTAAATGATAGAAATCAAAAGCTT	602
Db	645	CTTTAGAGCACACAATAATAAGGCCATCCATGATGTGAATGATCGGATACAGAGCGT	704
QY	603	GGGAGAGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCACTGTGCAAGCTCCCTGCTGA	662
Db	705	ATCCAGCTTTCAGTCAAGCTTTAGCTTAAGGCTGAGATCATCTTTCCAAGCTTTCAACCCGA	764
QY	663	CACACCATTACTCAAAATTTGCTTATAAATTTCAAGAGTGGGGCCCTGGAGAAAGGTTGGGG	722
Db	765	GACACCCTACTCTGAGTTTGAATATTTATTTCAAGGAATGGGTTTTCGCGAGGTTGGGG	824
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Db	825	CGATACTGCAGTACACGCTATTGGAGATGATGCACTCTCTCTTAGATATCTTCAAGCTCC	884
QY	783	AGACCCATCTACCTTAGAGAAATCTTTGGGGAGATCCCAATGATTTTAAAGTTGTTGT	842
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QY	843	GGTATCCCTCATGGATACITTTGCTCAAGCTTAATGTATTAGGCTTGCAGACACAGCAGG	902
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QY	963	AAAGAAACAGGGCTTCATGTTTCCCAAGATGTTCTCATTTGTTACTCGGCTGATACCAGA	1022
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QY	1083	CATATTAAGAGTTCCCTTCAGAAATGAAATGGGATATCTTAAGAAATGGATATCAAGATT	1142
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DEFINITION	<i>Solanum tuberosum</i> ; sucrose synthase mRNA, complete cds.		
ACCESSION	AY205302		

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VERSION      AY205302.1  GI:29289942
KEYWORDS
SOURCE       Solanum tuberosum (potato)
ORGANISM     Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE    1 (bases 1 to 2679)
AUTHORS      Loureiro,M., Kopka,J., Mueller-Roeber,B. and Trethewey,R.
TITLE        Characterization of effects of specific reduction in gene
              expression of two sucrose synthase genes in transgenic potato
              plants
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 2679)
AUTHORS      Kopka,J., Loureiro,M., Mueller-Roeber,B. and Trethewey,R.
TITLE        Direct Submission
JOURNAL      Submitted (20-DEC-2002) Plant Biology, Federal University of
              Vicososa, Av PH Rolfs S/N, Vicososa, MG 36570-000, Brazil
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ORIGIN

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Query Match      45.9%; Score 1264.8; DB 8; Length 2679;
Best Local Similarity 70.3%; Pred. No. 4.2e-202;
Matches 1711; Conservative 0; Mismatches 717; Indels 6; Gaps 1;

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VERSION
KEYWORDS AX507720.1 GI:23388957
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Harper, J.F., Kreps, J., Wang, X., and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing same, and methods of use
JOURNAL Patent: WO 0216655-A 2415 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG (CH)

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AY142511.1
KEYWORDS
FLI CDNA,
Arabidopsis thaliana (thale cress).

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE
AUTHORS

1 (bases 1 to 2506)
Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
Lee,J.M., Quach,H.L., Tang,C., Toriumi,M., Wallender,E.K., Wong,C.,
Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R.,
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Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE
JOURNAL

Arabidopsis Open Reading Frame (ORF) Clones
Unpublished

REFERENCE
AUTHORS

2 (bases 1 to 2506)
Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K.,
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Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE
JOURNAL

Direct Submission
Submitted (16-AUG-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA

COMMENT

The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and
sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yamada,K.,
Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M.,
Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C.,
Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Jones,T.,
Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T.,
Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.

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 VERSION
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 SOURCE
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 ORGANISM
 Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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 1 (bases 1 to 2898)
 Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
 Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,
 Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A.,
 Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X.,
 Miranda, M., Narusaka, M., Nguyen, V., Onodera, C.S., Palm, C.J.,
 Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A.,
 Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
 Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
 Arabidopsis cdna clones
 Unpublished
 2 (bases 1 to 2898)
 Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
 Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,
 Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A.,
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 Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A.,
 Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
 Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
 Direct Submission
 Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory
 (SIGAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN

Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H.,
 Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L.,
 Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G.,
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 Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
 Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
 this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
 contributed equally to this work as PIs.

FEATURES

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ORIGIN

Query Match 45.3%; Score 1249.8; DB 8; Length 2898;
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RESULT 14
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LOCUS

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DEFINITION Arabidopsis thaliana putative sucrose synthetase (At4g02280) mRNA, complete cds.

ACCESSION AY051001

VERSION AY051001.1

KEYWORDS GI:15293134

SOURCE FLI CDMNA

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 2904)

Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Mirada,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shimn,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Arabidopsis Full Length cDNA Clones

Unpublished

2 (bases 1 to 2904)

Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Gicag,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu.S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Mirada,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shimn,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission

Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu.S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Mirada,M., Nguyen,M., Palm,C.J., Shimn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

FEATURES

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3'UTR

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Zuechtungsforschung, Carl von Linne Weg 10, D-50829 Keeln, GERMANY

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Best Local Similarity 68.6%; Pred. No. 8e-188;			
Matches 1642; Conservative 0; Mismatches 744; Indels 6; Gaps 1;			
QY	32	GCATCCGGACCGCGTTCGAGGACACCCCTCCACGCGCACCGCAACGAGCTCGTGGCCCTCC	91
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DB	260	CTGAGGACGCAATGCTGAGGACCCCTGCAATAAAGAGCTGAGCGAGGCTTTTAATG	319
QY	206	ACGTCCTCCGCTCCGCGCAGGAGCGATCGTGTGCGCGCTTCGTGGCCATCGCGGTGC	265
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Qy	1586	CCATATTA	CTTTCCACATACCGAGAGCCAAAGCGACTCACTCTCTTTCAATG	1645
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Qy	1706	CAAAAGCCAT	CTCTTTCTCCATGGCAGAGCTTCGACAGGGTGAAGAAACATAACAGGGCTGG	1765
Db	1820	CGAAGCCATA	ATCTTCTCGATGCGAGGGCTTCGACCGSGTGAAGAACATCACTGGGCTGG	1879
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Db	1880	TTGAATGT	GTAGCCCAAGACAAANGCTGAGAGGCTCACAACTCGTGGTGGTGGCGG	1939
Qy	1826	GGTACAAT	GTATGTCAAACGTCGAAGCAGGGAAGAGATCGGGAGATAGAGAAGATGC	1885
Db	1940	GTTCACAC	GCCTGNAAGATTCGACGACAGAGGAGAGAGACGAGATAGAGAGATGC	1999
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Db	2000	ACAACTCAT	CGACCGATACCACTTGAAACGGAAGCTTGGGTGATATCTGCGCAGAGCA	2059
Qy	1946	ACAGGCGCG	TAAAGCGAGCTCTATCGCTACATCGCTGATACCCATGCTGCTTGGTAC	2005
Db	2060	ACAAAGCT	CGCAACGCGGAGCTCTACCGTTACATAGCTGACAAAGAGGGGATATTTGTGC	2119
Qy	2006	AGCGCGCT	TGTATGAAGCGTTGGTCTCACCGTGTGAGGCGCATGACCTGTGGGCTTC	2065
Db	2120	AGCTGCGT	TTTATGAAGCTTTTGGGCTTACGGTGTGAGGCGCATGACCTGTGGGCTTC	2179
Qy	2066	CTACTTT	CGCGAGCTCTCTGAGAGTCCAGCTGAGATCATAGAGCATGGCGTCTCGGCT	2125
Db	2180	CTCGGTTC	GCAACTCTCCAGCTGGGCGCCACAGAGATCATCGAAGACGGTGTCTCGGAT	2239
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Job time : 7069.61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 15:35:16 ; Search time 133.484 seconds
(without alignments)
11462.031 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

Sequence: 1 atgtctgcccgaagctgaa.....aaaaaaaaaaggggggccgc 2757

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	1131	41.0	3103	4	US-09-598-401C-57
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4	229.2	8.3	265	4	US-09-313-294A-1862
5	155	5.6	6386	2	US-08-483-376-1
6	142	5.2	532	4	US-09-598-401C-56
7	117.2	4.3	272	4	US-09-313-294A-1221
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13	89.8	3.3	3509	4	US-09-866-153-12
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42	52.6	1.9	1671	4	US-09-252-991A-1222	Sequence 1222, Ap
43	52.4	1.9	12001	1	US-08-458-568A-11	Sequence 11, Appl
44	51.6	1.9	1693	3	US-09-320-878-23	Sequence 23, Appl
45	51.6	1.9	1693	4	US-09-141-908-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-08-553-436A-7

Sequence 7, Application US/08553436A

Patent No. 5866790

GENERAL INFORMATION:

APPLICANT: HESSE, Holger

TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE

TITLE OF INVENTION: CONCENTRATION

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10036-8403

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,436A

FILING DATE: 17-NOV-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP94/01671

FILING DATE: 20-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 4317596.1

FILING DATE: 24-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Meilman, Edward

REGISTRATION NUMBER: 24,735

REFERENCE/DOCKET NUMBER: P/951-117

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 382-0700

TELEFAX: (212) 382-0888

TELEX: 236925

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2563 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Beta vulgaris

INDIVIDUAL ISOLATE: Saccharosynthesinase
 IMMEDIATE SOURCE:
 LIBRARY: phage lamda zap
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..2303
 US-08-553-436A-7

Query Match 42.7%; Score 1177.8; DB 2; Length 2563;
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Qy	244	CGGTCTGCGGCATCGCGTGGCGCGCGCGCGGAGTTGGAGTAGCTCGCGGTCAAC	303
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Qy	304	GTTCCAGAGCTCAGCTCGAGCAGCTCACAGTCTCGAGTACCTCCGCTTCAAGGAGG	363
Ds	141	GTCTCTGACTGATGTCGAGCAGCTAATCTGTCTGAGTATCTCCATTTCAAGGAAGAA	200
Qy	364	CTTGTGCGCGCCAGCAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGGTCAAT	423
Ds	201	CTTGTGCGATGGAAGGCTGATGACCACTATCTGCTTGAGCTTGATTTGAGCCCTTTAAT	260
Qy	424	GTCTCAGTCCCAAGCCCAATCGTCACTCATCTATTGGAAACGGTGTGAGTTCCTCAAC	483
Ds	261	GAATCAGTCCACGTCCAACTCGCTCTTCAATGGTATGGTGTTCAGTTCCTCAAT	320
Qy	484	CGACATGTTGCTCAATCATGTTCCGCAACAGGAGTTGTTGGAGCCCTCTGCGATTTC	543
Ds	321	CGGACCTGTGATCAGCATGTTCTGCAACAAAGATTGCTTGGAGCGGTACTTGAATTT	380
Qy	544	CTCGTGGCCACCGGCAAGAGGCGATGTTATGATGCTTAATGATAGATAACAAGCTTG	603
Ds	381	CTTAGAGTGCACAAACATAAAGGAGTTGTCATGATGTTGAATGATCGATACAGACTATC	440
Qy	604	GGGAGGCTCAGTCTGTCTGACCAAGCTGAGAGCAGTGTCAAAAGTCCCTGTGCTGAC	663
Ds	441	CAGGCTCTCAGTCTGCAATTTGTTAATCCAGAGTGGAGTATCTTATCAAACTTCAGCAGAT	500
Qy	664	ACACCATCTACAAATTTGCTTAATAATTTCAAGAGTGGCGCTGAGAAAGGTTGGGCT	723
Ds	501	ACACCTTACTCTGATTCGATTTGTTAATCCAGAGTATGGGTTTGAAGAGGCTGGGGT	560
Qy	724	GATACAGCAGGACATGTTTGGAAATGATCCATCTCTCTAGACATCATTCAGGCGCCA	783
Ds	561	GATACCTGCTGAAGAGGTTCTAGAAATGATGATGATGATGATGATGATGATGATGATGAT	620
Qy	784	GACCATCTACCTAGAGAAATCTGGGAGGATCCCGATGATTTTAACTGTTGTTGTTG	843
Ds	621	GATCCGTCTACATAGACATTTCTGGAAGAGTCTCCCATGTTGTTAATGTTGGTCAAT	680
Qy	844	GTATCCCTCATGATATCTTGGTCAAGCTTAATGATGATGATGATGATGATGATGATGATGAT	903
Ds	681	TTGCTGTCACATGATATTTTGAACAGGACATGTTGCTCGGCTGCTGATGATGATGATGATGAT	740
Qy	904	CAGATGCTCTATATCTAGCAAGTCCGTCGCTAGTAAATGAGATGTTCTCCGTTTA	963
Ds	741	CAGATGATTTATATATCTGACCAAGTCCGCTCTCTGMAACATGAATGCTCCCAACGAATA	800
Qy	964	AAGAAACAGGGCTTCATGTTTCCCAAGATTTCTATGTTACTCGGCTGATACAGAT	1023
Ds	801	AAGAACAGGACCTAGATGATCTCTAGAAATTTCTATGTTGATGATGATGATGATGATGATGAT	860
Qy	1024	GCAAAAGGACATCATGCAATCAGCGCTTGGAGAAATAGTGGACACAGCATACTTAC	1083
Ds	861	GCTTAAGGGACCACTGTCATCAAGCTATGGAGAAAGTCACTGGAACAGAGCATGCTAGT	920
Qy	1084	ATATTAGAGTTCCCTTTCAGAAATGAATGAGGATATCTTAAGAAATGGATATCAAGATT	1143

Ds	921	ATCCTGAGAGTTCCCTTTCCGATCAGAGAAAGAAATCCCTCCGAAATGGATATCTAGATT	980
Qy	1144	GATGTGTGCGCATATCTCGAAACATTTGCTGAGGATGCTGCTGGTGAATATGCTGCTGAA	1203
Ds	981	GATGTATGCGCTTATTTAGAGACCTTCACTGAGGATGAGCTGGTGAATATTTGGCGAG	1040
Qy	1204	TTAAGAAGTATCCAGACTTCATTAATTTGAAACTACAGTATGAGAAATCTTGTGGGCTCA	1263
Ds	1041	TTGCAAGGTCGTCAGATCTGATTAATTTGGCAACTACAGCGATGGAAATATAGTTGCTTCT	1100
Qy	1264	TGCTATCTTCAAGATCGGAATTTACCCAGTCCCAATTTGAGGACAAATATCACTTCTGCTGT	1323
Ds	1101	TTATTTGCCCAAAATGGGTGTACCCAGTGAATATAGCCCATGCAATTTGAGAAATCC	1160
Qy	1324	AAGTATCCAGATTCAGACATATTTTGGAAAGATTTGAGTGAAGTACCATTTCTCTCTGC	1383
Ds	1161	AAGTATCCAGATTCATTAATTTACTGGAAAGATTTGAGGACAAATATCACTTCTGCTGT	1220
Qy	1384	CAGTTCATCTGATTAATTTGCTATGAAACAAATGCTGATTTTATCATCAACAGCACATAC	1443
Ds	1221	CAATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1280
Qy	1444	CAAGAAATGCTGGAAGCAAAATACCTGTCGAGCAGTATGAGATCATACTGCTCTTACT	1503
Ds	1281	CAAGAGATAGCTGGAACGAGAAATACCTGTCGATTAATGAAAGCCATAAGGCTTTTACT	1340
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Ds	1341	TTTCCGGGCTGATTCGGGTGTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGAT	1400
Qy	1564	GTCTCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1620
Ds	1401	GTCTCTCTGAGGCGAGACATGGCCATCTACTTCCCATTTTTCAGAGAGAGATGTCACCTGT	1460
Qy	1621	CTCACTCTCTTTCATGTTCAATCGAAATTTTGAATTTATGATGATGATGATGATGATGATGATGAT	1680
Ds	1461	CTCACTCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1520
Qy	1681	CACATTTGGGATCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1740
Ds	1521	CACATTTGGTGTATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1580
Qy	1741	AGGTGAGAGACATTAACAGGCTGCTGAGAGCTTTTGGTAACTGATGATGATGATGATGATGATGATGAT	1800
Ds	1581	CGTGTGAAGATATAACAGGCTGCTGAGAGCTTTTGGTAACTGATGATGATGATGATGATGATGATGAT	1640
Qy	1801	CTGTAAACCTTGTGCTGCTTTCGGGCTACAAATGATGATGATGATGATGATGATGATGATGATGAT	1860
Ds	1641	CTGTAAACCTTGTGCTGCTTTCGGGCTACAAATGATGATGATGATGATGATGATGATGATGATGAT	1700
Qy	1861	GAGATCGCGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1920
Ds	1701	GAAATTTGCCAAATTCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1760
Qy	1921	TTCCGTGATCTCTGCGGAGACAAACAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT	1980
Ds	1761	TTTCCGTGATCTCTGCGGAGACAAACAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT	1820
Qy	1981	GCTGATACCCATGCTGCTTTCGGTACAGCGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT	2040
Ds	1821	TGTGACAAAGAGGATTTTTCGGGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1880
Qy	2041	GTTGAGGCGAT	2100
Ds	1881	GTTGAGGCGAT	1940
Qy	2101	ATCATAGACATGCGGCTCTCGGCTTCCCATTTGACCCGCTTACCATCCCGGACAGGCTGTT	2160
Ds	1941	ATTATAGAGACGCTGCTTTCAGGATTTTCAATTCGATTCATATCGATTCATGCTGATCAGGAGAA	2000
Qy	2161	AATCTGATGCGGCTTCTTTCGACCGGTCGAGAGAGCCAGATCACTGCTGGTGAATATA	2220

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Qy 2281 TTGATGACACTGGCGGGGTCTACGGTCTCTGGAAGTACGTGCGAAGCTCGAGGGCTG 2340
Db 2118 TTAATGACATTCGCGAGGGTGTATGGTCTCTGGAATATGTCTTAACTAGAGAGA 2177
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Db 2178 GAGACACGAGTATCTTGGAGATGTCTACATTTGAGGTTCGGTATCGGCTGACCT 2237
Qy 2401 GTGCGGCTTGGCAATTGACCAACGC 2425
Db 2238 GTTCGCTGGCAACAGATGAGAGC 2262

RESULT 2
US-09-598-401C-57
; Sequence 57, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C2
; CURRENT APPLICATION NUMBER: US/09/598,401C
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 3103
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-57

Query Match 41.0%; Score 1131; DB 4; Length 3103;
Best Local Similarity 56.9%; Pred. No. 5.5e-278;
Matches 1624; Conservative 0; Mismatches 800; Indels 3; Gaps 1;

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Db 447 ATGCTGATCGCATGTGTGACTCGAAGCCACAGCTTCGCGAGCGCTTTCGAGAGACCCCTC 506
Qy 61 CACGCGCACCGCAACGAGCTCGTCCGCTCTCTCCAGTACGTGAACAAAGGGAAGGSC 120
Db 507 TCTGCTCACCAGCATATGTGGCTCTCTCTCAGGGTTGAGCCAAAGGCAAGGC 566
Qy 121 ATCTGAGCGGCAACACATCTCGACGCTCGACGAGGTCGAGGCTCCGGGGTCCGC 180
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Qy 241 CCGCGCTTCTGTCGCTATCGGCTCGCGCGCGCGGAGTTTCGGAGTACGTCGCGCTC 300
Db 687 CTTCCATGGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 746
Qy 301 AACGTTCAAGGCTCAGGCTCAGGAGCTCAGCTCTCGGAGTACCTCCGCTTCAAGGAG 360
Db 747 AACGTTCAAGGCTTGTCTTGAAGCAATTGAGGAGTTCGCTGAGTATCTGCATCTCAAGAA 806

Qy 361 GAGCTTGTGAGCGCCAGACAAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGGTTTC 420
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Qy 421 AATGCTCAGTCCAGCGCCCAATCGGTCACTCATCTATTATGGAACGCTGTCAGTTCTTC 480
Db 867 ACTGCTCTTTTCCGCGCCGAGCTCTTTCCAACTTATTGGCAATGGCGTCGAGTTTCTC 926
Qy 481 AACCAGACACTTGTCTCTCAATCATGTTCGCAACAGAGGATTTGCTTGGAGCCCTCTGTCAT 540
Db 927 AATGCCATCTCTCCGCTAAGCTCTTCATGACAGAGAAAGCTTTCACCTCTGCTTGA 986
Qy 541 TTCTCCCTGGCCACCGGCAAGGGGCAATGTTATGATGCTTAAATGATGAATACAAAGC 600
Db 987 TTCTCCCAAGTCCACTGCTACAAAGGGGAAGAACATGATGTTGAATCCAGAAATCCAGAAT 1046
Qy 601 TTGGGGAGGCTTCACTCTGCTGTGCTGACCAAGCTGAGGAGCACTTGTCAAAGCTTCCCTGCT 660
Db 1047 GTGTTCTCCCTCCAACTGCTCTGAGAGGGGAGGAGTATCTGACCTCGCTCAAAACC 1106
Qy 661 GACACACCATACTCAAAATTTGCTTATAAATTTCAAGAGTGGGGCTCGAGAAAGGTTGG 720
Db 1107 GAGACCCGCTACTCCGAGTTCGAGCAAGTTCAGGAGATCGGGCTCGAGCGGGGTGG 1166
Qy 721 GGTGATACAGAGGACATGTTTTTGGAAATGATCCATCTCTCTTAGACATCATTCAGGG 780
Db 1167 GGTGACAGGCTGAGCGCTCTCGAGATGATCCAGCTCTCTGTTGGATCTCTCTTGAAGCT 1226
Qy 781 CCAGACCCATCTACCTCAGAGAAATCTTGGGAGGATCCCATGATTTTAACTGTTGT 840
Db 1227 CCGGACCCGTGCACTCTCGAAGGTTCTTGGATAGGGTTCCCATGTTCTTCAAGCTGCTG 1286
Qy 841 GTGGTATCCCTCATGATACCTTGTCAAGCTTAATGATTTAGGCTTGCACAGACAGGA 900
Db 1287 ATCATGCTCTCCACAGTACTTGTCTCAGGAGAGCTCTTGGTTATCGGATACCGGT 1346
Qy 901 GGACAGATGCTCTATATCTGACCAAGTCTGTGCACTAGAAATGAGATGTTCTTCCTG 960
Db 1347 GCGCAGGTTGTTTACATCTGATCAAGTTCGTGCTCCTAGAGAGAAATGCTTCAACCGC 1406
Qy 961 TTAAGAAACAGGCTGATGCTTCCCAAGATTTCTATGTTACTCGGCTGATACA 1020
Db 1407 ATTAAGCAACAGGACTGATATCTCTCGATTTCTCATTTACTCTCGGCTTCTTCCA 1466
Qy 1021 GATGCAAAAGGAACATCATGCAATCAGCGGCTTGAGAGAAATTAGTGAACACAGATACT 1080
Db 1467 GACGCGGTTGGAACCACTGTGCGCAGCGCTTGAAGAAAGTTTTTGGGACCGAGTACTCC 1526
Qy 1081 TACATATTACAGTTCCTCTGAAATGAAATGGAATGGAATGGAATGGAATGGAATGGAAT 1140
Db 1527 CACATTTCTCGGCTCCCTTCAAGAAATGAGAGGGAGTCTGCGCAAGTGAATTTCCCGG 1586
Qy 1141 TTTGATGTTGCGCCATATCTGAAACATTTCTGAGGATGCTGCTGTTGAATTTGCTGCT 1200
Db 1587 TTTGAGGTTGCGCCATTTTGAAGATGATCTGAGGATGTCGCGAGCGAACTTCTGGA 1646
Qy 1201 GAATTAAGGTAATCTCAGACTTCTATAATGGAATGGAATGGAATGGAATGGAATGGAAT 1260
Db 1647 GAGTTGCAAGGCAAGCTGATCTGATCATCGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1706
Qy 1261 TCATTTGCTCTTTCAGATGGAATTAACCAAGTGAACATTTGCTCATGCTCTGGAAG 1320
Db 1707 TCTTTGTTAGCAATAAATTAGTGTTCACAGATGATACATAGCCCATGCTCTCGAGAG 1766
Qy 1321 ACTAAGTATCCAGATTCAGATATTTTGGAGAGATTTTCGATGAGAACTACATTTCTCC 1380
Db 1767 ACAGAGTACCAGAGTCAAGATATCTGGAAGAAATTTGAGGAAAGATGACCATTTCTCT 1826
Qy 1381 TGCCAGTTTCACTGCTGATATAATTTGATGAACATGCTGATTTTATCATCACCAGCACA 1440
Db 1827 TGCCAGTTTCACTGCTGATCTCATGCCCATGAACCAACCGACTTCTATTCACCGACCC 1886

QY	- 441	TACCAAGAAATTCCTGGAAACAAAATATCTGTGTCGACAGTATGAGAGTCTATATCTGCTTTT	1500
Db	- 887	TTCAAAGAAATTCCTGGAAACAAAGATACAGTGGGGCAGTATGAGAGTCTCATCAAACTTC	1946
QY	1501	ACTCTGCTCTGTCTGTACCGAGTTGTCATGGGATCGATGCTTCTCGATCCAAAGTTCAAT	1560
Db	- 947	ACTCTTCTCGACTCTACCGAGTTGTCACGAGTCAGCTTCTTCGACCGAGTTCCAC	2006
QY	1561	ATAGTCTCTCTGGAGCTGCACATGTCCATATATCTTTCCATATCCGAGAAAGGCCAAGCGA	1620
Db	2007	ATTGTTTCAACAGTGTGACATGAGCATCTACTTTGCTTACACCGAAACAGGAGCGCGG	2066
QY	1621	CTGACCTCTCTCATGCTTCACTCGAAAATTTGATTTATGACCGCGAGCAAAACGATGAA	1686
Db	2067	TTGAATCTCTTCAACCTCGAGATCGAGAACTCTCTTTCAGCGATGTTGAGAAACAAGGAA	2126
QY	1681	CACATTTGGGCATCTGGATGATCCGGTCAAAGCCCATCTCTTCTCCATGGCAGAACTCGAC	1740
Db	2127	CACTTGTGTGTGTAAGATAAGAGAGCCCTATTATTTTACCATTGGCAGGCTGGAC	2186
QY	1741	AGGTTGAAGAAACATAACAGGGCTGTGTCGAAGCTTTTGTCTAAGTCGCTAAGCTGAAGGAG	1800
Db	2187	CGTGTCAAGAACTTGAACAGGCTTGTGTAGTGTGATGSCAAGAACTCCAAGTTGAGGAA	2246
QY	1801	CTGGTAAACCTCTCTGCTGTTCCGGTCAATGATGTCACAAAGTCCAAAGTCCAGACAGGAA	1860
Db	2247	CTCGCCACCTTGTCTGTGTTGGAGTGAACGGA---GGAAGGATTCGAGGACTTTGGA	2303
QY	1861	GAGATCCGGAGATAGAGAAATGCTATGAACCTCATCAAGACCCCAACAACTTTGTCGGCGAG	1920
Db	2304	GAGCAGTCTGAGATGAAGAAAATGTCAGACCTCATCGAAAAGTACAAGCTGATGATGCCAG	2363
QY	1921	TTCCGCTGGATCTCTGCCCHAGAACACAGGGCCCGTAAACGGCGAGCTCTATTCGTACATC	1980
Db	2364	TTCAGGTGGATTTCTCTCCAGATGAACCGGGTGAGGAAATGGAAGAGTCTTACCCTGACA-C	2423
QY	1981	GCTGATACCCATCGTCTTCGTPACAGCGCGCTGTGTAGAAGCGTTCCGTCTCCACCGTC	2040
Db	2424	TGTGAACAGAGGAGTCTCTGTTCAACCGCTATCTATGAAGCTTTCCGGTTGACCGTG	2483
QY	2041	GTTGAGCCCATGACCTGTGCGCTTCTCTACTTTTCGCGACGCTCCATGAGAGTCCAGCTGAG	2100
Db	2484	GTTGAGGCCATGACTTGTGGATTGCCAACTTTGCCACTTGCAATGTGACACAGCTGAG	2543
QY	2101	ATCATAGACATGGGCTCTCGGGCTTCCAGCTTGAACCCGTACCAACCCGHAACGGCTGTT	2160
Db	2544	ATCAITGTGATGGCAAAATCGGGCTACCAATGTATCTTACCAATGTCACGAGCGGCC	2603
QY	2161	AAFTCTGATGCCACTTCTTCGACCGGTCAACCAAGACCCAGATCACCTGGGTGAATATA	2220
Db	2604	GAGCTTCTTGTAGACTTCTTCAACAGTGCAGATTTGACCGCTCCACTGGGACGAGATC	2663
QY	2221	TCGGAAGCAGGGCTGCAGCGCATATACGAGAAATACACATGGAAGATATATCTCAGAGAGG	2280
Db	2664	TCAAGGGTGCCATGCAGAGAAATTTGAAGAGAGATATACATGGAAAAATATTTCTGAGAGG	2723
QY	2281	TTGATGACACTGSCCGGGTCTACGGTTCTCGAACTTACGTGTGAGAGCTCGAGAGGCTG	2340
Db	2724	CTG-TGAACCTGACTCCCGTGTATGGCTTCTGGAAGCATGTGACTAACTTGTATCGGGC	2783
QY	2341	GAGACGAGCGCTTACCTTGAGATGTTTCTACATCTGAAAGTTCGGCGAGCTGGCGAAGAC	2400
Db	2784	GAGAGTCGCGGTTACTTGAATGTTTCTATGCCCTCAAGTATCGCCCATCTGGCAAGTCT	2843
QY	2401	GTGCCGCTTGCAATTCACCAACCGCAG	2427
Db	2844	GTTCCTCCGGCTGTCCAGTAAACAAAG	2870

GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Buikema, William J.
APPLICANT: Bauer, Christopher C.
TITLE OF INVENTION: BACTERIAL SUCROSE SYNTHASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 443
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,005
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARSB:508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-684-005-1

Query Match	17.5%; Score 482.8; DB 4; Length 2700;
Best Local Similarity	53.7%; Pred. No. 6.3e-113;
Matches 1075; Conservative	0; Mismatches 912; Indels 15; Gaps 3
QY	375 CCAGCAAAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGGTTCAATGTCTCAGTCCC 434
Db	
QY	604 CCATCCCTTATGAAGCGGATATATTAGAACTAGATTTTCGGCCCTTCTACGATTACACCC 663
Db	
QY	435 ACGCCCCAAATCGGTCATCATCTATTGGAAAACGGGTGTCAGTTCTCTCAACCGACACTTGTC 494
Db	
QY	564 AACCATCGCGATCCCAGGAATATTGCAAGGGTGTCAATATCTTCAACCGTTATCTCTC 723
Db	
QY	495 CTCAAATCANGTTCGGCAACAGG---GATTGCTTGGAGCCCCGTGTGGATTTCCTCCGGTGG 551
Db	
QY	724 CAGTAAACTTTTTCAAGACTCGCAACAATGGCTGGAAAGTCGTTTAATTTCTTGCGCCT 783
Db	
QY	552 CCACCGGCACAGGGGCATGTTATGATGCTTTATGATAGAAATCAAAAGCTTGGGAGGCT 611
Db	
QY	784 ACATAATTACAATGGTATTCAACTACTATAAACCATCAAAATTCNAATCAAGCAACAAT 843
Db	
QY	612 TCAGTCTGTGCTGACCAAAAGCTCAGGAGCACTTGTCAAAGCTCCCTGCTGCACACACATA 671
Db	
QY	844 ATCAGAGCAAGTTAAAAACCGCGTTAACTTTGTGAGCGATCGGCCCAATGATGAACCCTA 903
Db	
QY	672 CTCACAAATTTGCTTTATAAATTTTCAAGAGTGGGGCCTGGAGAAAGTTGGGGTGCATACAGC 731
Db	
QY	904 CGAACAAATTCGGCTGCACTACAAACTATGGGTTTGAAGCGGGTGGGGTGTATACGCG 963
Db	
QY	732 AGGACATGTTTTCGAAATGATCCATCTCCCTTCTAGACATCAITTCAGCGCGCAGACCCCATC 791
Db	
QY	964 TTCTCTGTGTGGGGATACCTTAAACATTTTGGATGAATGATTGACTCTCCCGACCCCA 1023
Db	
QY	792 TACCCTAGAGAAATCTTGGGGAGGATCCCATGATTTTATAACGTTGTGTGTATCCCC 851
Db	
QY	1024 AACCCCTGGAAGCTTTTATCTCTCGCATCCGATGATTTTCAGAAATGCTCTAGTTTCAGC 1083
Db	

QY 852 TCATGATACCTTTGGTCAAGCTAATGTATTAGGCTTTGCCAGACACAGGAGGACAGATCGT 911
Db 1084 CCACGGTGGTTCCGACACAGAGGGGGTTTATGCTCGTCAAGATACCTGGTGGTCAAGTAGT 1143
QY 912 CTATATATCTGGACCAAGTCCGTGCACTAGAAATGAGATG-----GTTCTCCGTTT 962
Db 1144 GTAGCTCTTCCACCAAGCTAAGAAATTTAGAAAAGCACTGCAAGAAGATGCCATATCTGC 1203
QY 963 AAAGAAACAAGGGCTTGATGTTTCCCAAGATTTCTCATGTTACTCGGTGATACACAGA 1022
Db 1204 AGGTTTAGAGGATTTGAACGCTCCAGCCCAAGGTAATTAATCTCCACCCGCTCTGATTCCTAA 1263
QY 1023 TSCAAAAGGAACATCATCAATCAGCGCTTGAGAGAAATAGTGAACACACAGCATACTTA 1082
Db 1264 TAGTGAGGACCGCTTGTATACCAAGGTTAGAAAAGTCTACGGTACAGAGACCGCTG 1323
QY 1083 CATATTAGGAGTCCCTTCAGAAATGAAATGGGATCTTA---AGAAATGGATATCAAG 1139
Db 1324 GATTTGCGTGTACCTCTCGCGGAGTTTAAACCCCAAGATGACGCAAGTGGATTTCTCG 1383
QY 1140 ATTTGATGTGGCCACATCTGGAAACATTTGCTGAGGATCGCTGCTGTGAAATTTGCTGC 1199
Db 1384 ATTCGAGTTTGGGCTTATCTAGAAACCTTTGCCATTCGACTCAGAAAAGAGAAATTTGTGCG 1443
QY 1200 TGAATTACAAGGTACTCCAGACTTCATAATTTGGAACACTACAGTGTGATGAAATCTGTGCG 1259
Db 1444 AGAATTCAGAGTAGACAGACTTANTGCTGGGTAAATTAATCTAGCGGAACTTAGTTGC 1503
QY 1260 GTCATTTGCTTACAAAGATGGGAATPACCCAGTGCACAAATGCTCATGCTCTGGAAAA 1319
Db 1504 TTTTCTGTGACGCGGAGTAAAGTTACCCATGCAACATCGCTCATGCTTTAGAAAA 1563
QY 1320 GACTAAGTATCCAGATTCAGACATATTTTGAAGAAATTCGATGAGAAGTACCATTTCTC 1379
Db 1564 ATCCAAATCTGTTTGTAGTAACTTACTGCGCAAGATTTGGAAGAAAATATCATTTCTC 1623
QY 1380 CTGCCAGTTCACTGCTGATATAATTTGCTATGAACAATGCTCATTTTATCATCACCGAC 1439
Db 1624 TTTACAAATTCAGCGCTGATTTAATAGCTATGAATGCTGCTAACHTCTGTCATCACAGGAC 1683
QY 1440 ATACCAAGAAATTCCTGGAGCAAAAATATCTGTTGGAAGTATGAGATGATCATCTGCTT 1499
Db 1684 CTATCAAGAAATTTGTGGCACACCCAGACAGTATAGGCGAGTATGAGTCTTACAAATGCTT 1743
QY 1500 TACTTGCCTGCTGTGACCGAGTTGCTCATGCAATGCTGCTTCGATCCAAAGTTCAA 1559
Db 1744 TACATGCGGAACTGTATCATGTTGGTCAAGCGCAATTTGAATTTATTTAGCCCCCAATTTAA 1803
QY 1560 TATAGTCTCTCTGGAGCTGACATGTCCATATATCTTTCCACATACCGAAGGCCAAGCG 1619
Db 1804 CGTTGTACCGCTGTGTGAATGAABATTCCTACTTTCCCTACACAAACTCAAAACAG 1863
QY 1620 ACTCACTCTCTTCATGTTTCAATGCAAAATTTGATTTATGACCCGAGCAAAACGATGA 1679
Db 1864 ATAGAAAAGCGATCGGATCGCTTAGAGGAAATGCTGTTTACCCCTAGAAGATCTAGCCA 1923
QY 1680 ACACATTTGSCCATCTGATACCGGTCAAGGCCATCTCTTCTCCATGCGAAGCTCGA 1739
Db 1924 ATCTTTGCGCAAACTGCACGCCCAATTAAGGCTCTTAATTTTCTCAATGGCGGACTTGA 1983
QY 1740 CAGGGTGAAGAAATACAGGGCTGTGCGAAGCTTTTGTGTAAGTGGCGCTAAGCTGAGGA 1799
Db 1984 CCGAATTAATAAATCTCACAGTTTGGCGAAATGCTTTGGTCAAGTCAAGATTTGCAAGA 2043
QY 1800 GCTGGTAACCTTGTGCTGCTGCGGGTCAATATGATGTCAACAAAGTCCAAAGGACAGGA 1859
Db 2044 ACCTTGCAACTTAATTTAGTTGCAAGTAAAGCTGCGTATCGAAGATCAGAAGATACGA 2103
QY 1860 AGAGATCGCGGATAGAGAGATGATGAATCTCATCGAAGCCCAACACTTTGTTGGGCA 1919
Db 2104 AGAAAAGACGAAATCGTCAAACTTTACCGGATTTATTTGAGCAATATCAACCTCGCATGSCAA 2163

QY 1920 GTTCGGTGGATCTCTGCCAGACAAACAGGGCCCCCTAAGCGGAGCTCTATCGCTACAT 1979
Db 2164 AATTCGCTGTTAGGTGTGCGCTTATCCAAAAATGACTCCGGTGAATTTATCGCGTCAT 2223
QY 1980 CGCTGATACCCATGCTGCTTTCGTACAGCCGGCTGTGATGAGCGTTCGGTCTCACCGT 2039
Db 2224 TTGCGATCGCCAAAGGCAATTTTGTACAGCCAGCATTTATTGAGGCTTTGGGGTTGCAAT 2283
QY 2040 CTTGAGGCAATGACCTCTGGGCTTCTACTTTTCGCAAGCTCCATGGAGGTCAGCTGA 2099
Db 2284 CCTGGAGTCAATGATTTCCGGATTTGCCAATTTGCTACCCCAATTTGGGGGCCATTGGA 2343
QY 2100 GATCATAGAGATGCGGTCTCGGCTTCCCAATTTGACCCGTACACCCCGCAACAGGCTGT 2159
Db 2344 GATTATTCAAGGATAAGATTAATGGGCTTTACATTAACCTTACTCATCTAGAGAAACAGC 2403
QY 2160 TAACTGATGGCCGACTTCTTCGACGGTGCAGCAAGCAAGCAAGCAAGTCACTGGGTGATAT 2219
Db 2404 CACAAAATTTCTGATTTTCGTACCAAAATGCGAACAATTCCTAATTTTGAACATAAT 2463
QY 2220 ATCTGGAGAGGCTGCGAGCGCATATACGAGAAAGTACACATGGAAGATATATCTCAGAGAG 2279
Db 2464 TTCCGAGAAAGCCATTGACAGAGTATATAGTACATACACCTCGAAAATACACACACTAA 2523
QY 2280 GTTGATGACATGCGCGGGTCTAGGCTTTCTGGAAGTACGCTGCAAGCTCGAGAGGCT 2339
Db 2524 GCTGTAACTTGTAGCTCGGATTTACGGCTTCTGGAATTTTACTCGAAAAGAAAACGCGA 2583
QY 2340 GGAGACGAGGCGCTACCTTTGAG 2361
Db 2584 AGATTTATTACGCTACCTTTGAG 2605

RESULT 4

US-09-313-294A-1862
; Sequence 1862, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1862
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551647H1
US-09-313-294A-1862

Query Match 8.3%; Score 229.2; DB 4; Length 265;
Best Local Similarity 95.9%; Pred. No. 7.1e-49;
Matches 257; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 474 GTTCCTCAACCGACACTGTGCTCAATCATGTTCCGCAACAGGATGCTTGGAGCCCT 533
Db 1 GTTCCTCAACCGACACTGTGCTCAATCATGTTCCGCAACAGGATGCTTGGAGCCCT 60
QY 534 GTTGGATTTCTCGTGGCCACCGGCAAGGGGCGCATGTTATGCTTATGATGATGAT 593
Db 61 GCTGGATTTCTCGTGGCCACCGGCAAGGGGCGCATGTTATGATGCTT-ATGATGAT 119
QY 594 ACAAGCTTGGGAGGCTTCCAGTCTGTGCTGACCAAAAGCTGAGGACACTTGTCAAAGCT 653
Db 120 ACAAGCTTGGGAGGCTTCCAGTCTGTGCTGACCAAAAGCTGAGGACACTTGTCAAAGCT 179
QY 654 CCTGCTGACACACCTACTCATCAATTTGCTTATAAATTTCAAGAGTGGGCGCTTGAGAA 713

Db 180 CCCGCTGACACACATACATCAGATTGCTTATTAATTTTCAGAGTGGGGC--TGGAGA 237

Qy 714 AGGTGGGGTATACAGCAGGACATGTT 741

Db 238 AAGTGGGGTATACAGCAGGACATGTT 265

RESULT 5

US-08-483-376-1
; Sequence 1, Application US/08483376
; Patent No. 595330
; GENERAL INFORMATION:
; APPLICANT: Vasil, Vimla
; APPLICANT: Clancy, Maureen A.
; APPLICANT: Ferl, Robert J.
; APPLICANT: Vasil, Indra K.
; APPLICANT: Hannah, L. C.
; TITLE OF INVENTION: No. 595330el Means for Enhancing Gene
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,376
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,540
; FILING DATE: 07-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,115
; FILING DATE: 04-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/830,956
; FILING DATE: 05-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/353,854
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Dorna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 10-94B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: ENA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; STRAIN: Black Sweet
; FEATURE:
; NAME/KEY: exon
; LOCATION: 131..182
; FEATURE:
; NAME/KEY: exon

; LOCATION: 1211..1324
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1828..1948
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2041..2187
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2269..2460
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2605..2728
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2822..3038
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3256..3351
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3447..3620
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3702..3818
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3912..4078
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4158..4381
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4517..4835
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4768..5212
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5372..5510
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5636..5917
; US-08-483-376-1

Query Match 5.6%; Score 155; DB 2; length 6386;
Best Local Similarity 70.5%; Pred. No. 3e-29;
Matches 222; Conservative 0; Mismatches 90; Indels 3; Gaps 1;

Qy 1693 CTGGATGACCGGTCAAGGCCATCCTCTTCTCCATGGCAAGACTCGACAGGGTGAAGAAC 1752
Db 4524 CTGAAGGACAAAGAAAGCCGATCATCTTCTCGATGGCGGTCTCGACCGCGTGAAGAAC 4583
Qy 1753 ATACAGGGGCTGGTTCGAAGCTTTTGTAACTAGGCTAAGCTGAGGGAGCTGGTAAACCTT 1812
Db 4584 ATGACAGGCTGGTTCGAAGTGTACGGCAAGAACCGCGCTGAGGGAGCTGGCGAACCTC 4643
Qy 1813 GTGCTGTTCCCGGGTACAAATGATGTCAACAAGTCCAAAGACAGGGGAAGAGATCGCGGAG 1872
Db 4644 GTGATGTTCCCGGTGAC---CAAGCAAGAGTCCAAAGGACAGGGAGGAGGAGCGGAG 4700
Qy 1873 ATAGAGAAGATGATGAATCATCAAGACCCCAACTTTTTCGGGCAATTTTCGGCTGGATC 1932
Db 4701 TTCAAGAAGATGTACAGCTTCATCGACGAGTCAAGTTGAAGGGGCCATATCCCGTGGATC 4760
Qy 1933 TCTGCCACAGCAACAGCGGCCCGTAAACGGGAGCTCTATCGCTACATCGCTGTATACCCAT 1992
Db 4761 TCGGCGCAGATGAACCGCGTCCGCAAGCGGAGCTGTACCGCTACATTTCCGATACGAG 4820
Qy 1993 GGTGCTTTGATACAG 2007
Db 4821 GGCGCATTCGTGACG 4835

```
RESULT 6
US-09-598-401C-56
; Sequence 56, Application US/09598401C
; Patent No. 6596325
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C2
; CURRENT APPLICATION NUMBER: US/09/598.401C
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Pas-Seq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-598-401C-56

Query Match
Best Local Similarity 5.2%; Score 142; DB 4; Length 532;
Matches 229; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 1 ATGTCGCCCGGAGCTGACCGCAACGCGAGCATCCGGGACCGGTCGAGGACACCCCTC 60
Db 158 ATGCTGATCGCATGTTGACTCGAAGCACAGCTTCGCGAGCGTTTGACGAGACCCCTC 217

QY 61 CAGCGCACCGGACGAGCTCGTCCGCTCTCTCCAAAGTACGTAACGAGGGAAGGC 120
Db 218 TCTGCTCACCACGACGATATGTGCGCTCTCTTCAAGGGTTGAAGCCAGGGCAAGGC 277

QY 121 ATCTGACGCGGACCAACATCTCGACGCGCTCGACGAGGTCGAGGGCTCCGGGGTCGC 180
Db 278 ATCTGACGCGGACCAACATCTCTGAGTTGAGGCGCATCTCTGAGGAGGACGAGCA 337

QY 181 GCGCTCGCGGAGGACCTCTCTGAGCTCTCTCGCTCCGCGAGGAGTTGCGGAGTACGTCGGCTC 240
Db 338 AGCTTCTGATGCGGCTTTGTTGAAGTCTCTAAATCCACTCAGGAGGAGTGTGTCG 397

QY 241 CGCGCGTTCGTCGCAATCGCGTGCAGGCTCGAGGAGTTGCGGAGTACGTCGGCTC 300
Db 398 CTTCCATGGGTTGCTTGTGTTGTTCCAAAGCGCGGCGTGTGGAGCAGCATCGTGTG 457

QY 301 AAGTTTACAGCTCAGCTCGAGGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 360
Db 458 AAGTTCATCGCTGTTGTTGAGCAATGAGAGTGTGCTGAGTATCTGCACTTCAAGAA 517

QY 361 GAGCTTGTGACGG 374
Db 518 GAGCTTGTGATGG 531

RESULT 7
US-09-313-294A-1221
; Sequence 1221, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14

Query Match
Best Local Similarity 4.1%; Score 111.8; DB 4; Length 271;
Matches 178; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

QY 889 CCGACACAGGAGGACAGATCGTCTATATCTGACCAAGTCCGTCACATAGAAAATGAG 948
Db 2 CCGACACAGGAGGACAGATCGTCTATATCTGACCAAGTCCGTCACATAGAAAATGAG 61

QY 949 ATGCTTCTCGGTTTAAAGAAACAGGCTTGATGTTTCCCAAGATCTCTATTTTACT 1008
Db 62 ATGCTTCTCGGTTTAAAGAAACAGGCTTGATGTTTCCCAAGATCTCTATTTTACT 121

QY 1009 CGGCTGATACAGATGCAAGGAAACATCATGCAATCAGCGGCTTGAGAGAAATAGTGA 1068
Db 1009 CGGCTGATACAGATGCAAGGAAACATCATGCAATCAGCGGCTTGAGAGAAATAGTGA 1068

; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1826
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551585H1
US-09-313-294A-1826

Query Match
Best Local Similarity 4.3%; Score 117.2; DB 4; Length 272;
Matches 181; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 1466 ATACTGTGAGCAGTATGAGAGTCACTACTGCTTTACTCTGCTGCTGCTGCTGCTGCTGCTG 1525
Db 4 ACACCGTGGGCGAGTACGAGTCCCAATCGCGTTCACCTCTCTGCTGCTGCTGCTGCTGCTGCTG 63

QY 1526 TCCATGGGATCGATGCTCTTCGATCCAAAGTTCAATATAGTCTCTCTGAGCTGAGCATGT 1585
Db 64 TCCATGGGATCGATGCTCTTCGATCCAAAGTTCAACATTTGCTCTCCCTGAGCAGACATGA 123

QY 1586 CCATATACTTTCCACATACCGAGAGGCAAGCGACTCACCTCTCTTCAATGTTCAATCG 1645
Db 124 GTGTTTACTACCGTTHACGGA-AACGACAGAGACTCACTGCTTCCATCTCTGAAATCG 182

QY 1646 AAAATTGATTTATGACCCCGAGGACAAACGATGAACACATTGGGCTGATGATGACCGGT 1705
Db 183 AGGAGCTCATCTACAGCGAGCTCGAGAACTCGAGCACAAGTTCTGCTGAGGACACAGA 242

QY 1706 CAAGCCCATCTCTCTCTCCATGCGCAAGAC 1735
Db 243 AGAAGCCGATCATCTCTCTGATGCGCGCTC 272

RESULT 8
US-09-313-294A-1826
; Sequence 1826, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1826
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551585H1
US-09-313-294A-1826

Query Match
Best Local Similarity 4.1%; Score 111.8; DB 4; Length 271;
Matches 178; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

QY 889 CCGACACAGGAGGACAGATCGTCTATATCTGACCAAGTCCGTCACATAGAAAATGAG 948
Db 2 CCGACACAGGAGGACAGATCGTCTATATCTGACCAAGTCCGTCACATAGAAAATGAG 61

QY 949 ATGCTTCTCGGTTTAAAGAAACAGGCTTGATGTTTCCCAAGATCTCTATTTTACT 1008
Db 62 ATGCTTCTCGGTTTAAAGAAACAGGCTTGATGTTTCCCAAGATCTCTATTTTACT 121

QY 1009 CGGCTGATACAGATGCAAGGAAACATCATGCAATCAGCGGCTTGAGAGAAATAGTGA 1068
Db 1009 CGGCTGATACAGATGCAAGGAAACATCATGCAATCAGCGGCTTGAGAGAAATAGTGA 1068
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Db 122 AGTTGCTCCCTGATGCACTGGCAACCACTGTGGCCAGCGCTTGAGAAAGTCTCTGGC 181
 QY 1069 ACACAGCATACTTACATATTACGAGTTCCTTCAGAAATGAAATGGATCTTAAGAA 1128
 Db 182 AC-CGGCACTGCCATATCTTCGGTGCCATTCAGAACAGAAACGGGAATCGTTGGCA 240
 QY 1129 TGGATATCAAGATTGTATGTGGCCATATC 1159
 Db 241 TGGATCTCGCATTTGAAGTCTGGCCGTACC 271

 RESULT 9
 US-08-175-471-6
 ; Sequence 6, Application US/08175471
 ; Patent No. 5665892
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Assche, C.
 ; APPLICANT: Lando, D.
 ; APPLICANT: Bruneau, J.M.
 ; APPLICANT: Voelker, T.
 ; TITLE OF INVENTION: Sucrase Phosphate Synthase (SPS), Its
 ; TITLE OF INVENTION: Process For Preparation, Its cDNA, and Utilization of cDNA To
 ; TITLE OF INVENTION: Modify The Expression Of SPS In The Plant Cells
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Calgene, Inc.
 ; STREET: 1920 Fifth Street
 ; CITY: Davis
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 95616
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 6.0.7
 ; SOFTWARE: Microsoft Word 4.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/175,471
 ; FILING DATE: 27-DEC-1993
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/672,646
 ; FILING DATE: 18 MAR 1991
 ; APPLICATION NUMBER: EP 90402084.9
 ; FILING DATE: 20 JUL 1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elizabeth Lassen
 ; REGISTRATION NUMBER: 31,845
 ; NAME: Donna E. Scherer
 ; REGISTRATION NUMBER: 34,719
 ; REFERENCE/DOCKET NUMBER: CGNE 72-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (916) 753-6313
 ; TELEFAX: (916) 753-1510
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3509 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 US-08-175-471-6

 Query Match 3.3%; Score 89.8; DB 1; Length 3509;
 Best Local Similarity 51.0%; Pred. No. 8.8e-13;
 Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;
 QY 1678 GAACACATTTGGGCACTGATGACCGGTCAAGCCCATCTTCTTCCATGGCAAGACTC 1737
 Db 1543 GAAGTATCGGTTCTCTGACCAACCTCAAGCCGATGATCTGCGTTATCAAGACCA 1602
 QY 1738 GACAGGGTGAAGACATACAGGGCTGTGGAAGCTTTGTAGTGCCTAGCTGAGG 1797

Db 1603 GACCCGAGAGAACATCACTACCTCTGTCARAGGTTTGGAGAGTGTGCTCCACTCAGG 1662
 QY 1798 GAGCTGGTAAACCTTGTCTGTTGCCGGGTACAAATGATGTCAAAGTCCAGGACAGG 1857
 Db 1663 GAACTTGCMAACCTTACTCTGATCATGGTTAAACAGAGATGACATCGACGATGTCTGCT 1722
 QY 1858 GAAGAGATCGCGAGTAGAAGATGATCAATCACTCTCAAGACCCCAACACTTGTTCGGG 1917
 Db 1723 GGCAATGCCAGTGTCTCCACACAGATTCTGAAGCTGATTGACAAAGTATGATCTGTACCG- 1781
 QY 1918 CAGTTCCGCTGGATCTCTGCCCAGACAAACAGGGCCCGCTAACGGGAGCTCTATCGCTAC 1977
 Db 1782 --AAGCTGGCGTTCCCTAAGCATCACAATCAGGCTGAGTCCCGGAGATCTATCGCCTC 1839
 QY 1978 ATCGCTGATACCCATGGTGTCTTCTGTCACGCGGCTTGTATGAAGCGTTTGGTCTCACC 2037
 Db 1840 GCGGCCAAATGAAGGGCGTCTTCATCAACCTGCTCTGTTGAGCCGCTTTGGTCTCACC 1899
 QY 2038 GTCGTTGAGGCCATGACCTGTGGGCTTCTCTACTTTTGGGAGCTCCATGGAGGTCCAGCT 2097
 Db 1900 CTGATCGAGGCTGCGGCACACGAGTCTCCGATAGTCTGCTACCAAGATGGTGGTCCGTC 1959
 QY 2098 GAGATCATAGACATGCGGCTTCGCGGCTTCCACATTTGACCGGTACCCGTCACC 2146
 Db 1960 GACATTACAAATGCATTAAACACGAGCTGCTGTTGACCCACACGACC 2008

 RESULT 10
 US-08-718-777-6
 ; Sequence 6, Application US/08718777
 ; Patent No. 5981852
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Assche, C.
 ; APPLICANT: Lando, D.
 ; APPLICANT: Bruneau, J. M.
 ; APPLICANT: Voelker, T.
 ; APPLICANT: Gervais, M.
 ; TITLE OF INVENTION: MODIFICATION OF SUCROSE
 ; TITLE OF INVENTION: PHOSPHATE IN PLANTS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Barbara Rae-Venter
 ; STREET: 260 Sheridan Avenue, Suite 440
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/718,777
 ; FILING DATE: NOT YET ASSIGNED
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/175,471
 ; FILING DATE: 27-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barbara Rae-Venter
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.072.020S
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)328-4400
 ; TELEFAX: (415)328-4477
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3509 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear


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; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 112..3315
US-08-718-777-5

Query Match          3.3%; Score 89.8; DB 2; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1678 GAACACATTGGGCAATCTGGATGACCGGTCAAGGCCCATCTCTTCTCCATGGCAGACATC 1737
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1738 GACAGGTGAAGAAATACAGGGGTGCTCGAAGCTTTTGTAACTGCGCTAAGCTGAGG 1797
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1603 GACCCGAAGAAGACATCACTACCTCGTCAAGGCTTTGGAGAGTGTCTCCACTCAGG 1662
QY 1798 GAGCTGTAAACCTTGTCTGTTCGCGGTACAAATGATGTCAACAAAGTCCAGGACAGG 1857
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1663 GAACCTTGCAAACTTACTCTGATCATGGGTAAACAGAGATGACATCGACATGTCTGCT 1722
QY 1858 GAAGAGATCGCGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1917
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1723 GGCATGCGCACTGCTCACCACAGTCTGAAGCTGATGACAAAGTATGATCTGTACGG- 1781
QY 1918 CAGTTCGCGTGGATCTCTGCCACAGAAACAGGGCCCGTAAAGCGGAGCTCTATCGCTAC 1977
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1782 --AAGCGTGGCGTTCCCTAAGCNCATCAGCTGAGCTGCCGAGATCTATCGCTC 1839
QY 1978 ATCGTGATACCCATGCTTGTGATAGAGAGATGATGATGATGATGATGATGATGATGATG 2037
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1840 GCGGCCAAATGAAGGGGCTTTCATCAACCTGCTCTCGTGAAGCCGTTTGGTCTCACC 1899
QY 2038 GTGCTGAGGCCATGACCTGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2097
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1900 CTGATCGAGGCTGGGCACACAGGACTCCGATAGCTGCTGATCAAGAAATGTTGGTCCGTC 1959
QY 2038 GAGATCATAGAGCATGGGCTTCGCGCTTCCACATGACCGGTACCC 2146
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1960 GACATTACAAATGATTAACAAGGACTGCTGTTGACCCACAGGACC 2008

RESULT 11
US-09-078-862-2
; Sequence 2, Application US/09078862
; Patent No. 6091003
; GENERAL INFORMATION:
; APPLICANT: Nan, Guo-Ling
; APPLICANT: Nagai, Chifumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
; TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,862
; FILING DATE: 14-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UH-03321
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-078-862-2

Query Match          3.3%; Score 89.8; DB 3; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1678 GAACACATTGGGCAATCTGGATGACCGGTCAAGGCCCATCTCTTCTCCATGGCAGACATC 1737
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1543 GAAGTGATGCGGTCTCTGACCAACCTCTCAAGCCGATGATCTCTGGCGTTATCAAGACCA 1602
QY 1738 GACAGGTGAAGAAATACAGGGGTGCTCGAAGCTTTTGTAACTGCGCTAAGCTGAGG 1797
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1603 GACCCGAAGAAGACATCACTACCTCGTCAAGGCTTTGGAGAGTGTCTCCACTCAGG 1662
QY 1798 GAGCTGTAAACCTTGTCTGTTCGCGGTACAAATGATGTCAACAAAGTCCAGGACAGG 1857
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1663 GAACCTTGCAAACTTACTCTGATCATGGGTAAACAGAGATGACATCGACATGTCTGCT 1722
QY 1858 GAAGAGATCGCGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1917
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1723 GGCATGCGCACTGCTCACCACAGTCTGAAGCTGATGACAAAGTATGATCTGTACGG- 1781
QY 1918 CAGTTCGCGTGGATCTCTGCCACAGAAACAGGGCCCGTAAAGCGGAGCTCTATCGCTAC 1977
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1782 --AAGCGTGGGCTTCCCTAAGCNCATCAGCTGAGCTGCCGAGATCTATCGCTC 1839
QY 1978 ATCGTGATACCCATGCTTGTGATAGAGAGATGATGATGATGATGATGATGATGATGATG 2037
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1840 GCGGCCAAATGAAGGGGCTTTCATCAACCTGCTCTCGTGAAGCCGTTTGGTCTCACC 1899
QY 2038 GTGCTGAGGCCATGACCTGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2097
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1900 CTGATCGAGGCTGGGCACACAGGACTCCGATAGCTGCTGATCAAGAAATGTTGGTCCGTC 1959
QY 2038 GAGATCATAGAGCATGGGCTTCGCGCTTCCACATGACCGGTACCC 2146
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1960 GACATTACAAATGATTAACAAGGACTGCTGTTGACCCACAGGACC 2008

RESULT 12
US-09-051-341-6
; Sequence 6, Application US/09051341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,341
; FILING DATE:
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Thu May 27 10:13:55 2004

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17351
; FILING DATE: 25-OCT-1996
; APPLICATION NUMBER: US 08/549,016
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,200
; FILING DATE: 12-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter, Ph.D.,
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.110.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 112..3315
; US-09-051-341-6

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Query Match 3.3%; Score 89.8; DB 3; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1678 GAACACATTGGGCATCTGGATGACCGGTCAAGCCCATCTCTTCTTCCATGGCAAGACTC 1737
DB 1543 GAAGTGATCGGTTCTGACCAACCTCTCAAGCCGATGATCTCTGCGTTATCAAGACCA 1602

QY 1738 GACAGGTTGAAGACATATACAGGGCTGGTGGAGCTTTTGTCTAAGTGGCTAAGCTGAGG 1797
DB 1603 GACCCGAAAGAACATCATCACTACCTCGTCAAAGCGTTTGGAGAGTGTGCTCCACTCAGG 1662

QY 1798 GAGCTGGTAAACCTTGTGCTGTCGCGGTACAAATGATGTCAACAAAGTCCAAAGGACAGG 1857
DB 1663 GAATTTGCAACCTTACTCTGATCATGGTAAACAGAGATGACATCGACGACATGTCTGCT 1722

QY 1858 GAAGAGATCGCGAGATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1917
DB 1723 GGCATGTCAGTGTCTCTACCAACCTCTCAAGCCGATGATCTCTGCGTTATCAAGACCA 1602

QY 1918 CAGTTCGGTGGATCTCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 1797
DB 1603 GACCCGAAAGAACATCATCACTACCTCGTCAAAGCGTTTGGAGAGTGTGCTCCACTCAGG 1662

QY 1782 --AAGCGTGGCGTTCCTTAAGCATCAATCAGGCTGAGTCCCGGAGATCTATCGCTC 1839
DB 1798 ATCGCTGATACCATGCTTTCGTACAGCCGCGCTTGTATGAAGCGTTCGGTCTCACC 2037
DB 1840 GCGGCCAAATGAAGGCGTCTTCATCAACCTGCTCTCGTTGAGCGGTTTGGTCTCACC 1899

QY 2038 GTGTTGAGGCCATGACCTGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2097
DB 1900 CTGATCGAGCTCGGCGACACAGGACTCCCGATAGTCCCTACCAAGATGTTGGTCCGGTC 1959

QY 2098 GAGATCATAGAGCATGGCGTCTCGGCTTCCCATTTGACCCGATACCAACC 2146
DB 1960 GACATTACAATGCAATTAACACGAGTCTCTGTTGACCCACACGACC 2008

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RESULT 13
US-09-866-153-12
; Sequence 12, Application US/09866153
; Patent No. 6638766
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF

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; FILE REFERENCE: US-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-866-153-12

Query Match 3.3%; Score 89.8; DB 4; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1678 GAACACATTGGGCATCTGGATGACCGGTCAAGCCCATCTCTTCTTCCATGGCAAGACTC 1737
DB 1543 GAAGTGATCGGTTCTGACCAACCTCTCAAGCCGATGATCTCTGCGTTATCAAGACCA 1602

QY 1738 GACAGGTTGAAGACATATACAGGGCTGGTGGAGCTTTTGTCTAAGTGGCTAAGCTGAGG 1797
DB 1603 GACCCGAAAGAACATCATCACTACCTCGTCAAAGCGTTTGGAGAGTGTGCTCCACTCAGG 1662

QY 1798 GAGCTGGTAAACCTTGTGCTGTCGCGGTACAAATGATGTCAACAAAGTCCAAAGGACAGG 1857
DB 1663 GAATTTGCAACCTTACTCTGATCATGGTAAACAGAGATGACATCGACGACATGTCTGCT 1722

QY 1858 GAAGAGATCGCGAGATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1917
DB 1723 GGCATGTCAGTGTCTCTACCAACCTCTCAAGCCGATGATCTCTGCGTTATCAAGACCA 1781

QY 1918 CAGTTCGGTGGATCTCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 1977
DB 1782 --AAGCGTGGCGTTCCTTAAGCATCAATCAGGCTGAGTCCCGGAGATCTATCGCTC 1839

QY 1978 ATCGCTGATACCATGCTTTCGTACAGCCGCGCTTGTATGAAGCGTTCGGTCTCACC 2037
DB 1840 GCGGCCAAATGAAGGCGTCTTCATCAACCTGCTCTCGTTGAGCGGTTTGGTCTCACC 1899

QY 2038 GTGTTGAGGCCATGACCTGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2097
DB 1900 CTGATCGAGCTCGGCGACACAGGACTCCCGATAGTCCCTACCAAGATGTTGGTCCGGTC 1959

QY 2098 GAGATCATAGAGCATGGCGTCTCGGCTTCCCATTTGACCCGATACCAACC 2146
DB 1960 GACATTACAATGCAATTAACACGAGTCTCTGTTGACCCACACGACC 2008

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RESULT 14
US-09-693-467A-12
; Sequence 12, Application US/09693467A
; Patent No. 6686513
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-04331
; CURRENT APPLICATION NUMBER: US/09/693,467A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-693-467A-12

Query Match 3.3%; Score 89.8; DB 4; Length 3509;
Best Local Similarity 51.0%; Pred. No. 8.8e-13;

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:31:02 ; Search time 689.979 Seconds
(without alignments)
16851.697 Million cell updates/sec

Title: US-10-080-114A-1
Perfect score: 2737
Sequence: 1 gtgaccaccgctccggcg.....aaaaaaaaaaggcgccgc 2737

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 3373863 seqs, 212409041 residues
Word size : 50

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 29Jan04: *
1: geneseqn1980s: *
2: geneseqn1980s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002s: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2737	100.0	2737	6	Aad45849 Corn suc
2	2571	93.9	2757	6	Aad45856 Corn Sus3
3	278	10.2	428	8	Aad58861 Maize suc
4	255	9.3	303	8	Aad58379 Maize suc
5	209	7.6	283	8	Aad58372 Maize suc
6	192	7.0	297	9	Aad58886 Corn DNA
7	191	7.0	258	9	Aad58843 Corn DNA
8	159	5.8	285	8	Aad58359 Maize suc
9	158	5.8	297	8	Aad58362 Maize suc
10	150	5.5	150	8	Aad58373 Maize suc
11	143	5.2	411	8	Aad58864 Maize suc
12	134	4.9	255	8	Aad58374 Maize suc
13	130	4.7	181	8	Aad58370 Maize suc
14	122	4.5	265	7	ABX83402 Corn ear-
15	114	4.2	310	8	Aad58369 Maize suc
16	99	3.6	148	8	Aad58371 Maize suc
17	85	3.1	347	6	Aad45857 Sorghum p
18	83	3.0	137	8	Aad58375 Maize suc
19	63	2.3	264	8	Aad58368 Maize suc

ALIGNMENTS

```
RESULT 1
AAD45849
ID AAD45849 standard; cDNA; 2737 BP.
XX
AC AAD45849;
XX
DT 27-DEC-2002 (first entry)
XX
DE DE
XX Corn sucrose synthase (Sus3) cDNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KW cellulose; corn; Sus3; gene; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
CDS 2..2410
FT /*tag= a
FT /product= "Corn Sus3 protein"
XX
PN WO200267662-A1.
XX
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG, Niu X;
XX
XX WPI; 2002-691625/74.
XX
XX P-PSDB; AAE28499.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Claim 1; Page 102-103; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is corn Sus3 cDNA
XX
XX Sequence 2737 BP; 711 A; 672 C; 697 G; 657 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2737; DB 6; Length 2737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGACCCACGCTCCGGGACCGGCTCGAGGACACCTCCACGCGCACCGACGAGCT 60
Db 1 GTGACCCACGCTCCGGGACCGGCTCGAGGACACCTCCACGCGCACCGACGAGCT 60
Qy 61 CGTGGCCCTCTGTCCCAAGTACGTGAACAGGGGCAAGGGCATCTCGAGCGCGCACCAT 120
Db 61 CGTGGCCCTCTGTCCCAAGTACGTGAACAGGGGCAAGGGCATCTCGAGCGCGCACCAT 120
Qy 121 CCTGACGCGCTCGACGAGGTCCAGGGGCTCCGGGGGGCGCGCTAGCGAGGACCCCTT 180
Db 121 CCTGACGCGCTCGACGAGGTCCAGGGGCTCCGGGGGGCGCGCTAGCGAGGACCCCTT 180
```

181 QY CCTCGAGCTCCTCCGCTCCGCGAGGAGCGATCGTGTGCTGCGCCGCTTGGTGGCCATCGC 240
181 DB CCTCGAGCTCCTCCGCTCCGCGAGGAGCGATCGTGTGCTGCGCCGCTTGGTGGCCATCGC 240
241 QY GGTGCGCCGCGCCGCGAGTTGGAGTACGTCCGCGTCAACGTTCAACGAGCTCAGCGT 300
241 DB GGTGCGCCGCGCCGCGAGTTGGAGTACGTCCGCGTCAACGTTCAACGAGCTCAGCGT 300
301 QY CGAGCAGCTCACAGTCTCGAGTACCTCCGCTTCAAGGAGGAGCTTGTGCGACGCGCAGCA 360
301 DB CGAGCAGCTCACAGTCTCGAGTACCTCCGCTTCAAGGAGGAGCTTGTGCGACGCGCAGCA 360
361 QY CAATGATCCCTAGTCTCGAGTTCGAGTTCGAGCCGTTCAATGTCTCAAGTCCCAAGCC 420
361 DB CAATGATCCCTAGTCTCGAGTTCGAGTTCGAGCCGTTCAATGTCTCAAGTCCCAAGCC 420
421 QY AAATCGGTCAATCATCTAATGGAAACGGTGTGCAAGTTCCTCAACCGGACACTTGTCTCAAT 480
421 DB AAATCGGTCAATCATCTAATGGAAACGGTGTGCAAGTTCCTCAACCGGACACTTGTCTCAAT 480
481 QY CATGTTCCGGAACAGGAGTGTGAGGCCCTGTTGGATTTCCTCCGTGGGCCACCGGCA 540
481 DB CATGTTCCGGAACAGGAGTGTGAGGCCCTGTTGGATTTCCTCCGTGGGCCACCGGCA 540
541 QY CAAGGGCATGTTATGATGCTTAATGATAGATAACAAAGCTTGGAGGCTTCAAGTCTGT 600
541 DB CAAGGGCATGTTATGATGCTTAATGATAGATAACAAAGCTTGGAGGCTTCAAGTCTGT 600
601 QY GCTGACAAAGCTGAGGAGCACTTGTCAAGCTCCCTGCTGACACACCACTACTCAAAAT 660
601 DB GCTGACAAAGCTGAGGAGCACTTGTCAAGCTCCCTGCTGACACACCACTACTCAAAAT 660
661 QY TGTCTATAAATTTCAAGAGTGGGCTCGGAGAAAGTTGGGGTGTACACAGGACATGT 720
661 DB TGTCTATAAATTTCAAGAGTGGGCTCGGAGAAAGTTGGGGTGTACACAGGACATGT 720
721 QY TTTGGAATGATCTCTCTCTACACATCATTTAGGCGCCAGACCCATCTACCCCTAGA 780
721 DB TTTGGAATGATCTCTCTCTACACATCATTTAGGCGCCAGACCCATCTACCCCTAGA 780
781 QY GAAATTTCTGGGAGGATCCCATGATTTTAAAGTTGTTGGTATCCCTCATGGATA 840
781 DB GAAATTTCTGGGAGGATCCCATGATTTTAAAGTTGTTGGTATCCCTCATGGATA 840
841 QY CTTTGGTCAAGCTAATGATTAAGCTTGGCAGACACAGGAGGACAGATCGTCTATATCT 900
841 DB CTTTGGTCAAGCTAATGATTAAGCTTGGCAGACACAGGAGGACAGATCGTCTATATCT 900
901 QY GGACCAAGTCCGTGCACTAGAAAATGAGATGTTCTCCGTTTAAAGAAAACAGGGCTTGA 960
901 DB GGACCAAGTCCGTGCACTAGAAAATGAGATGTTCTCCGTTTAAAGAAAACAGGGCTTGA 960
961 QY TGTTCCTCCAAAGATCTCATTTTACTCGGCTGATACAGATGCAAAAGGAACATCATG 1020
961 DB TGTTCCTCCAAAGATCTCATTTTACTCGGCTGATACAGATGCAAAAGGAACATCATG 1020
1021 QY CAATCAGCGCTTGAGAGAAATAGTGGAAACACAGCATCTTACATTAATAGGATTCCTT 1080
1021 DB CAATCAGCGCTTGAGAGAAATAGTGGAAACACAGCATCTTACATTAATAGGATTCCTT 1080
1081 QY CAGAAATGAATGGGATACCTTAAGAAATGGATATCAAGATTTGATGTGGCCATATCT 1140
1081 DB CAGAAATGAATGGGATACCTTAAGAAATGGATATCAAGATTTGATGTGGCCATATCT 1140
1141 QY GGAACATTTGTGAGAGTGTGCTGGTGAATTTGCTGTAATTAAGGTAATCCAGCA 1200
1141 DB GGAACATTTGTGAGAGTGTGCTGGTGAATTTGCTGTAATTAAGGTAATCCAGCA 1200
1201 QY CTTTCAATTTGAAACACAGTATGGAATCTTGTGGGCTGATTTGCTATCTTCAAGAT 1260
1201 DB CTTTCAATTTGAAACACAGTATGGAATCTTGTGGGCTGATTTGCTATCTTCAAGAT 1260

1261 QY GGAATTTACCCAGTCAACATTCCTCATCTCTGGAAGAGACTAAGTATCCAGATTGAGA 1320
1261 DB GGAATTTACCCAGTCAACATTCCTCATCTCTGGAAGAGACTAAGTATCCAGATTGAGA 1320
1321 QY CATATTTTGAAGAAATTTTCGATGAGAAATACCAATTTCTCTGCGAGTTCATCTGTATAT 1380
1321 DB CATATTTTGAAGAAATTTTCGATGAGAAATACCAATTTCTCTGCGAGTTCATCTGTATAT 1380
1381 QY AATGCTATGAACAATGCTGATTTTATCATCAACAGACATACCAAGAAATTTGCTGAAG 1440
1381 DB AATGCTATGAACAATGCTGATTTTATCATCAACAGACATACCAAGAAATTTGCTGAAG 1440
1441 QY CAABAATACCTGTTGAGACAGTATGAGAGTCAATGCTTTTACTCTGCTGCTGCTGACCG 1500
1441 DB CAABAATACCTGTTGAGACAGTATGAGAGTCAATGCTTTTACTCTGCTGCTGCTGACCG 1500
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1501 DB AGTTGTCCATGGATCGATGTTCTTCGATCCAAAGTTTCAATATAGTCTCTCTGAGCTGA 1560
1561 QY CATGTCATATATCTTTCCATACACGAGAGGCGAAGGACTCACTCTCTCTCTCATGTTTC 1620
1561 DB CATGTCATATATCTTTCCATACACGAGAGGCGAAGGACTCACTCTCTCTCTCATGTTTC 1620
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1681 QY CCGGTCAAAGCCCATCTCTTCTTCATGCAACACTCGACAGGCTGAAGAACATAACAGG 1740
1681 DB CCGGTCAAAGCCCATCTCTTCTTCATGCAACACTCGACAGGCTGAAGAACATAACAGG 1740
1741 QY GCTGTCGAAGCTTTTGTCTTAAGTCGCTTAAGTGAAGGAGCTGGTAAACCTTGTGCTGT 1800
1741 DB GCTGTCGAAGCTTTTGTCTTAAGTCGCTTAAGTGAAGGAGCTGGTAAACCTTGTGCTGT 1800
1801 QY TGCCTGATCAATGATGTCAACAAAGTCCAGAGACAGGAGAGATCCGAGAGATAGAGAA 1860
1801 DB TGCCTGATCAATGATGTCAACAAAGTCCAGAGACAGGAGAGATCCGAGAGATAGAGAA 1860
1861 QY GATGCTGAATCAATCAAGACCAACAACTTGTTCGGGCGAGTTCGCTGGATCTCTGCCCA 1920
1861 DB GATGCTGAATCAATCAAGACCAACAACTTGTTCGGGCGAGTTCGCTGGATCTCTGCCCA 1920
1921 QY GACAAACAGGCGCGCTTAAGCGAGCTCTATGCTGATCTATGCTGATACCACTGCTGCTT 1980
1921 DB GACAAACAGGCGCGCTTAAGCGAGCTCTATGCTGATCTATGCTGATACCACTGCTGCTT 1980
1981 QY CGTACAGCGCGCTTGTATGAAGCTTCGCTCTACCGCTGTTGAGGCGCATGACCTGTGG 2040
1981 DB CGTACAGCGCGCTTGTATGAAGCTTCGCTCTACCGCTGTTGAGGCGCATGACCTGTGG 2040
2041 QY GCTTCTACTTTTCGAGCGCTCCATGAGGCTCCAGCTGAGATCATAGAGCATGGCGTCTC 2100
2041 DB GCTTCTACTTTTCGAGCGCTCCATGAGGCTCCAGCTGAGATCATAGAGCATGGCGTCTC 2100
2101 QY GGGCTTCCCATTTGACCGCTTCAACCCCGAAACGCTGTTTAACTCTGATGGCGACTTCCT 2160
2101 DB GGGCTTCCCATTTGACCGCTTCAACCCCGAAACGCTGTTTAACTCTGATGGCGACTTCCT 2160
2161 QY CGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGAGCAGGGCTGCAGCG 2220
2161 DB CGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGAGCAGGGCTGCAGCG 2220
2221 QY CATATACGAGAGATACATGAGAGATATCTCAGAGAGGTTGATCACTGCGCGGGGT 2280
2221 DB CATATACGAGAGATACATGAGAGATATCTCAGAGAGGTTGATCACTGCGCGGGGT 2280
2281 QY CTACGGTTTCTGGAAGTACGTGTCGAAGCTCGAGAGGCTGGAGACGAGGCGCTACCTTGA 2340
2281 DB CTACGGTTTCTGGAAGTACGTGTCGAAGCTCGAGAGGCTGGAGACGAGGCGCTACCTTGA 2340
2341 QY GATGTTCTATACATGAAAGTTCCGCGAGCTGGCGAAGACCGTCCCGCTTSCAATTGACCA 2400

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Db 2341 GATCTCTACACTAGTTCCGCGAGCTGGCGAAGCGTGCCGCTTGCAATTGACCA 2400
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QY 2461 GACCTTCAGTAATTAGCGCGCGGAGAGCGGTAGCCATAAATGTGGCGAGCTGAACCTG 2520
Db 2461 GACCTTCAGTAATTAGCGCGCGGAGAGCGGTAGCCATAAATGTGGCGAGCTGAACCTG 2520
QY 2521 GTTTTATTATGATACATAATGGCAGATATAACAAATTAATCTGAAGCGAGGTGGGTGCGAG 2580
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QY 2581 TTGTGTGTTGCTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTG 2640
Db 2581 TTGTGTGTTGCTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTG 2640
QY 2641 GCAAGCGCGAGGCACTGGTGAAGTCTGATCAATATACATCATATTTCTGTTGACCTGTGAAA 2700
Db 2641 GCAAGCGCGAGGCACTGGTGAAGTCTGATCAATATACATCATATTTCTGTTGACCTGTGAAA 2700
QY 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGC 2737
Db 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGC 2737

RESULT 2
AAD45856
ID AAD45856 standard; DNA; 2757 BP.
AC
AC AAD45856;
XX
DT 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)
XX
DE Corn Sus3-Sorghum EST chimeric DNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KW cellulose; corn; Sus3; chimeric; gene; ds.
XX
OS Zea mays.
OS Sorghum propinquum.
OS Chimeric.
XX
Key Location/Qualifiers
CDS 1..2430
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FT misc_feature 1..39
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FT /note= "Sorghum propinquum EST DNA"
FT misc_feature 40..2757
FT /*tag= c
FT /note= "Corn Sus3 DNA"
XX
PN WO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG, Niu X;
XX
XX NPI; 2002-691625/74.
XX
XX P-PSDB; AAE28502.
XX

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PT New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving
PT plant or grain strength.
XX Claim 1; Page 116-119; 125pp; English.
XX
CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
CC acids. The polynucleotide, or its encoded protein, is useful for
CC modulating the level of sucrose synthase in a transgenic plant,
CC increasing cellulose production in the stalk tissue of a transgenic
CC plant or increasing the concentration of cellulose in the tissues of a
CC seed of a transgenic plant. This is particularly useful in plants of a
CC maize or soybean) breeding, especially for e.g. improving stalk length in
CC maize, reducing grain breakage during combining, transport or movement
CC into storage, or improving plant or grain strength. The present sequence
CC is Corn Sus3-Sorghum EST chimeric DNA. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;
Query Match 93.9%; Score 2571; DB 6; Length 2757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 GCCGAGGACCCCTTCCTCGACGCTCTCCGCTCCGCGCGAGGCGCATCGTCTGCCGCG 226
Db 187 GCCGAGGACCCCTTCCTCGACGCTCTCCGCTCCGCGCGAGGCGCATCGTCTGCCGCG 246
QY 227 TTCTGTGCGCATCGCGGTGCGCGCGCGCGCGAGTTTGGGAGTAGTCTCGCGTCAACGTT 286
Db 247 TTCTGTGCGCATCGCGGTGCGCGCGCGCGCGAGTTTGGGAGTAGTCTCGCGTCAACGTT 306
QY 287 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTT 346
Db 307 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTT 366
QY 347 GTGAGCGCGAGCACAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGCGTTCAATGTC 406
Db 367 GTGAGCGCGAGCACAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGCGTTCAATGTC 426
QY 407 TCAGTCCCGACGCCAAATCGGTTCATCTATTTGAAACGGTGTGTCAGTCTCTCAACCGA 466
Db 427 TCAGTCCCGACGCCAAATCGGTTCATCTATTTGAAACGGTGTGTCAGTCTCTCAACCGA 486
QY 467 CACTTGTCTCAATCATGTTCCGCAACAGGAGTGTCTTGGAGCCCTCTGTGGATTTCCTC 526
Db 487 CACTTGTCTCAATCATGTTCCGCAACAGGAGTGTCTTGGAGCCCTCTGTGGATTTCCTC 546
QY 527 CGTGGCCACCGGCAAGGGGCGATGTTATGATGCTTATGATAGATAGATACAAAGCTTGGG 586
Db 547 CGTGGCCACCGGCAAGGGGCGATGTTATGATGCTTATGATAGATAGATACAAAGCTTGGG 606
QY 587 AGGCTTCAGTCTGTGTCGACCAAAAGCTGAGCAGACATTGTCAAAGCTCCCTGCTCAGACA 646
Db 607 AGGCTTCAGTCTGTGTCGACCAAAAGCTGAGCAGACATTGTCAAAGCTCCCTGCTCAGACA 666
QY 647 CCATACCTCACAATTGTGCTTATAAATTTCAAGAGTGGGGCGCTCGAGAAAGGTTGGGGTGAT 706
Db 667 CCATACCTCACAATTGTGCTTATAAATTTCAAGAGTGGGGCGCTCGAGAAAGGTTGGGGTGAT 726
QY 707 ACAGCAGACATGTTTGGGAAATGATCCATCTCTCTAGACATCATTCAGGCGCGCAGAC 766
Db 727 ACAGCAGACATGTTTGGGAAATGATCCATCTCTCTCTAGACATCATTCAGGCGCGCAGAC 786
QY 767 CCATCTACCTTAGAGAAATCTTCGGGAGGATCCCATGATTTTAAAGCTTGTCTGTGTA 826
Db 787 CCATCTACCTTAGAGAAATCTTCGGGAGGATCCCATGATTTTAAAGCTTGTCTGTGTA 846
QY 827 TCCCTCATGATACCTTTGGTCAAGCTAACTATTTAGGCTTGGCCAGACACAGGAGGACAG 886
Db 847 TCCCTCATGATACCTTTGGTCAAGCTAACTATTTAGGCTTGGCCAGACACAGGAGGACAG 906

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D5 243 ACCGTCGCGCTGCATTCAGCAACGACGAGTACCTTGGCGCACTGCAGCTGCAGTACT 302
QY 2438 TGTGTACAGACTGAACCTGAAGGACCTTCAGTAATTTAGGCGCGGAGACGCTAGCCAA 2497
D5 303 TGTGTACAGACTGAACCTGAAGGACCTTCAGTAATTTAGGCGCGGAGACGCTAGCCAA 362
QY 2498 TAAATGTCCGCGAGCTGAAGTGGTTTTT 2526
D5 363 TAAATGTCCGCGAGCTGAAGTGGTTTTT 391

RESULT 4
ADA58379
ID ADA58379 standard; cDNA; 303 BP.
XX
AC ADA58379;
XX
DT 20-NOV-2003 (first entry)
XX
DE Maize sucrose synthase EST #23.
XX
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
OS Zea mays.
XX
PN US2003135870-AL.
XX
PD 17-JUL-2003.
XX
PF 26-JAN-1999; 99US-00237183.
XX
PR 24-NOV-1997; 97US-0067000P.
PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 10-FEB-1998; 98US-0074282P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
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PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077229P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.
PR 18-MAR-1998; 98US-0078368P.
PR 07-APR-1998; 98US-0080844P.
PR 27-APR-1998; 98US-0083067P.
PR 29-APR-1998; 98US-0083386P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
PR 29-APR-1998; 98US-0083390P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0099667P.
PR 09-SEP-1998; 98US-0099670P.
PR 09-SEP-1998; 98US-0099697P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
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PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
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PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX
(CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
PI Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX
XX New maize or soybean enzymes and nucleic acid molecules associated with
XX the sucrose pathway, useful for genome mapping, gene identification and
XX analysis, plant breeding, or preparation of constructs for plant gene
XX expression.
XX
XX Claim 2; Page; 117pp; English.
XX
XX The invention relates to a substantially purified nucleic acid molecule
XX (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
XX or its fragment, associated with the sucrose pathway selected from:
XX triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
XX 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
XX vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
XX fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
XX hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
XX glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
XX diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
XX substantially purified maize or soybean enzyme (or its fragment) and a
XX transformed plant having a nucleic acid molecule. Also disclosed as new
XX are purified antibodies capable of specifically binding to the maize or
XX soybean enzyme, determining a level or pattern of a plant sucrose pathway
XX enzyme in a plant cell or plant tissue, determining a mutation in a plant
XX whose presence is predictive of a mutation affecting the level or pattern

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CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX Sequence 303 BP; 71 A; 78 C; 86 G; 58 T; 0 U; 0 Other;

Query Match 9.3%; Score 255; DB 8; Length 303;
 Best Local Similarity 100.0%; Pred. No. 1.3e-90;
 Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1741 GCTGGTCAAGCTTTGCTAAGTCGGCTAAGTCAGGAGCTGTAACCTTGTGCTGCT 1800
 Db ||||| 1 GCTGGTCAAGCTTTGCTAAGTCGGCTAAGTCAGGAGCTGTAACCTTGTGCTGCT 60

QY 1801 TGCGGGTACAATGATGTCAACAGTCCAGGACAGGAGATCGCGAGATAGAGAA 1860
 Db ||||| 61 TGCGGGTACAATGATGTCAACAGTCCAGGACAGGAGATCGCGAGATAGAGAA 120

QY 1861 GATGATGAAGTATCAAGACCCCACTTTTCGGGAGTTCGGCTGGATCTTGCCCA 1920
 Db ||||| 121 GATGATGAAGTATCAAGACCCCACTTTTCGGGAGTTCGGCTGGATCTTGCCCA 180

QY 1921 GACAAACAGGCGCGTAAACGCGAGCTATCGCTACATCCGCTATCCATGCTGCTTT 1980
 Db ||||| 181 GACAAACAGGCGCGTAAACGCGAGCTATCGCTACATCCGCTATCCATGCTGCTTT 240

QY 1981 CGTACAGCGCGCTT 1995
 Db ||||| 241 CGTACAGCGCGCTT 255

RESULT 5

ADA58372

ID ADA58372 standard; cDNA; 283 BP.

XX ADA58372;

XX 20-NOV-2003 (first entry)

XX Maize sucrose synthase EST #16.

XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
 KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucosyltransferase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX Zea mays.

XX US2003135870-A1.

XX 17-JUL-2003.

XX 26-JAN-1999; 99US-00237183.

XX 24-NOV-1997; 97US-0067000P.

XX 09-DEC-1997; 97US-0069472P.

XX 27-JAN-1998; 98US-0072888P.

XX 10-FEB-1998; 98US-0074201P.

XX 10-FEB-1998; 98US-0074280P.

PR 10-FEB-1998; 98US-0074281P.
 PR 10-FEB-1998; 98US-0074282P.
 PR 12-FEB-1998; 98US-0074566P.
 PR 12-FEB-1998; 98US-0074567P.
 PR 19-FEB-1998; 98US-0074789P.
 PR 19-FEB-1998; 98US-0075459P.
 PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
 PR 19-FEB-1998; 98US-0075462P.
 PR 19-FEB-1998; 98US-0075463P.
 PR 19-FEB-1998; 98US-0075464P.
 PR 06-MAR-1998; 98US-0076912P.
 PR 09-MAR-1998; 98US-0077223P.
 PR 09-MAR-1998; 98US-0077230P.
 PR 09-MAR-1998; 98US-0077231P.
 PR 18-MAR-1998; 98US-0078368P.
 PR 07-APR-1998; 98US-0080844P.
 PR 27-APR-1998; 98US-0083067P.
 PR 29-APR-1998; 98US-0083386P.
 PR 29-APR-1998; 98US-0083387P.
 PR 29-APR-1998; 98US-0083388P.
 PR 29-APR-1998; 98US-0083389P.
 PR 29-APR-1998; 98US-0083390P.
 PR 13-MAY-1998; 98US-0085222P.
 PR 13-MAY-1998; 98US-0085223P.
 PR 13-MAY-1998; 98US-0085224P.
 PR 21-MAY-1998; 98US-0086183P.
 PR 21-MAY-1998; 98US-0086184P.
 PR 21-MAY-1998; 98US-0086185P.
 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089810P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
 PR 09-SEP-1998; 98US-0093667P.
 PR 09-SEP-1998; 98US-0093670P.
 PR 09-SEP-1998; 98US-0093677P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
 PR 21-SEP-1998; 98US-0101132P.
 PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108966P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.

(CHEI/) CHEIKH N.

PA (FISH/) FISHER D K.

PA (LIU/) LIU J.

XX Cheikh N, Fisher DK, Liu J;
 XX WPI; 2003-688722/65.
 XX New maize or soybean enzymes and nucleic acid molecules associated with
 PT the sucrose pathway, useful for genome mapping, gene identification and
 PT analysis, plant breeding, or preparation of constructs for plant gene
 PT expression.
 XX
 XX Claim 2; Page; 117pp; English.
 XX
 XX The invention relates to a substantially purified nucleic acid molecule
 CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
 CC or its fragment, associated with the sucrose pathway selected from:
 CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucosomerase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucosomase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
 CC transformed plant having a nucleic acid molecule. Also disclosed as new
 CC are purified antibodies capable of specifically binding to the maize or
 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
 CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
 CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.
 XX
 XX Sequence 283 BP; 75 A; 74 C; 67 G; 67 T; 0 U; 0 Other;
 SQ
 Query Match 7.6%; Score 209; DB 8; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1529 CCAAGTTCAATATAGTCTCTCTCGAGCTGACATGTCATATACITTCACATACCGAG 1588
 DB 9 CCAAGTTCAATATAGTCTCTCTCGAGCTGACATGTCATATACITTCACATACCGAG 68
 QY 1589 AAGCCCAAGGACTCACCTCTCTTCATGGTTCAATCGAATTTGATTTATGACCCGGAG 1648
 DB 69 AAGCCCAAGGACTCACCTCTCTTCATGGTTCAATCGAATTTGATTTATGACCCGGAG 129
 QY 1649 CAAACGATGAACACATTTGGGCATCTGGATGACCGGTCAAAGCCCATCTCTTCCCATG 1708
 DB 129 CAAACGATGAACACATTTGGGCATCTGGATGACCGGTCAAAGCCCATCTCTTCCCATG 188
 QY 1709 GCAAGACTCGACAGGGTGAAGAACATAAC 1737
 DB 189 GCAAGACTCGACAGGGTGAAGAACATAAC 217
 RESULT 6
 ADC08886/c
 ID ADC08886 standard; DNA; 297 BP.
 XX
 XX ADC08886;
 XX
 XX 18-DEC-2003 (first entry)
 XX
 XX Corn DNA sequence Seq ID:191 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 XX Zea mays.
 XX
 XX W02003000905-A2.
 XX
 XX 03-JAN-2003.
 XX
 XX 21-JUN-2002; 2002MO-1B002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 22-JUN-2001; 2001US-0325277P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 26-DEC-2001; 2001US-0342327P.
 XX
 XX (SVKN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Riecke D;
 PI
 DR WPI; 2003-229341/22.
 XX
 XX New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 PT
 XX Disclosure; SEQ ID NO 1191; 130pp; English.
 XX
 XX This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence from corn which showed homology to rice "grain filling"
 CC genes of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.
 XX
 XX Sequence 297 BP; 87 A; 57 C; 70 G; 83 T; 0 U; 0 Other;
 SQ
 Query Match 7.0%; Score 192; DB 9; Length 297;
 Best Local Similarity 99.6%; Pred. No. 9.2e-66;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1373 GCTGATATATTTGCTATGAACAATGCTGATTTTATCATCACCACATACCAAAATT 1432
 DB 243 GCTGATATATTTGCTATGAACAATGCTGATTTTATCATCACCACATACCAAAATC 184
 QY 1433 GCTGGAAGCAAAATATCTGTTGGACATGAGATCATCTGCTTTACTCTGCTGCT 1492
 DB 183 GCTGGAAGCAAAATATCTGTTGGACATGAGATCATCTGCTTTACTCTGCTGCT 124
 QY 1493 CTGTACCGAGTTGTCATGGATCGATGTTCTTCGATCCAAAGTTCAATATAGTCTCTCT 1552
 DB 123 CTGTACCGAGTTGTCATGGATCGATGTTCTTCGATCCAAAGTTCAATATAGTCTCTCT 64
 QY 1553 GGAGCTGACATGTCATATATCTTTCCCATACACCGAAGGCCAAGCGACTCACTCTCTT 1612
 DB 63 GGAGCTGACATGTCATATATCTTTCCCATACACCGAAGGCCAAGCGACTCACTCTCTT 4
 QY 1613 CAT 1615
 DB 3 CAT 1

PR 19-FEB-1998; 98US-0075464P.
 PR 06-MAR-1998; 98US-0076912P.
 PR 09-MAR-1998; 98US-0077223P.
 PR 09-MAR-1998; 98US-0077230P.
 PR 09-MAR-1998; 98US-0077231P.
 PR 18-MAR-1998; 98US-0078368P.
 PR 07-APR-1998; 98US-0080844P.
 PR 27-APR-1998; 98US-0083067P.
 PR 29-APR-1998; 98US-0083386P.
 PR 29-APR-1998; 98US-0083387P.
 PR 29-APR-1998; 98US-0083388P.
 PR 29-APR-1998; 98US-0083389P.
 PR 29-APR-1998; 98US-0083390P.
 PR 13-MAY-1998; 98US-0085222P.
 PR 13-MAY-1998; 98US-0085223P.
 PR 21-MAY-1998; 98US-0085224P.
 PR 21-MAY-1998; 98US-0086183P.
 PR 21-MAY-1998; 98US-0086184P.
 PR 21-MAY-1998; 98US-0086185P.
 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089800P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
 PR 09-SEP-1998; 98US-0098657P.
 PR 09-SEP-1998; 98US-0099670P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101330P.
 PR 21-SEP-1998; 98US-0101331P.
 PR 21-SEP-1998; 98US-0101332P.
 PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 23-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00119129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.
 XX (CHEZ/) CHEIKH N.
 PA (FISH/) FISHER D K.
 PA (LIU/) LIU J.
 XX Cheikh N, Fisher DK, Liu J;
 PT WPI; 2003-688722/65.
 XX
 PT New maize or soybean enzymes and nucleic acid molecules associated with
 PT the sucrose pathway, useful for genome mapping, gene identification and
 PT analysis, plant breeding, or preparation of constructs for plant gene
 PT expression.
 XX
 PS Claim 2; Page; 117pp; English.

XX The invention relates to a substantially purified nucleic acid molecule
 CC (appearing as ADA57847 - ADAG0660 that encodes a maize or soybean enzyme
 CC or its fragment, associated with the sucrose pathway selected from:
 CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
 CC are purified antibodies capable of specifically binding to the maize or
 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
 CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
 CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
 XX
 SQ Sequence 297 BP; 92 A; 51 C; 65 G; 89 T; 0 U; 0 Other;
 Query Match 5.8%; Score 158; DB 8; Length 297;
 Best Local Similarity 99.2%; Pred. No. 2.3e-52;
 Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1102 TAAGAAATGGATATCAAGATTGATGTGGCCATATCTGGAACATTTGCTGAGATGC 1161
 DB 2 TAAGAAATGGATATCAAGATTGATGTGGCCATATCTGGAACATTTGCTGAGATGC 61
 QY 1162 TGCTGGTGAATTCGCTGCTGAATTAACAAGTACTCCAGACTTCAATTTGGAATACAG 1221
 DB 62 TGCTGGTGAATTCGCTGCTGAATTAACAAGTACTCCAGACTTCAATTTGGAATACAG 121
 QY 1222 TGATGGAATTCGCTGGCGTCAATTCCTATCTTCAAGATGGGAATTACCCAGTCAACAT 1281
 DB 122 TGATGGAATTCGCTGGCGTCAATTCCTATCTTCAAGATGGGAATTACCCAGTCAACAT 181
 QY 1282 TGCTCATGCTCTGGAAGACTAAGTATCCAGATTCAGACATATTTGGAGAGATTTCGA 1341
 DB 182 TGCTCATGCTCTGGAAGACTAAGTATCCAGATTCAGACATATTTGGAGAGATTTCGA 241
 QY 1342 TGAGAGTACCAATTTCTCCT 1361
 DB 242 TGAGAGTACCAATTTCTCCT 261
 RESULT 10
 ADA58373
 ID ADA58373 standard; cDNA; 150 BP.
 XX
 AC ADA58373;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Maize sucrose synthase EST #17.
 XX
 KW Plant; sg; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
 KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;

KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.

OS Zea mays.

XX US200313587C-A1.

PN 17-JUL-2003.

PD 26-JAN-1999; 99US-00237183.

XX 24-NOV-1997; 97US-0067000P.

PR 09-DEC-1997; 97US-0069472P.

PR 27-JAN-1998; 98US-0072888P.

PR 10-FEB-1998; 98US-0074201P.

PR 10-FEB-1998; 98US-0074280P.

PR 10-FEB-1998; 98US-0074281P.

PR 12-FEB-1998; 98US-0074565P.

PR 12-FEB-1998; 98US-0074566P.

PR 12-FEB-1998; 98US-0074567P.

PR 19-FEB-1998; 98US-0074789P.

PR 19-FEB-1998; 98US-0075459P.

PR 19-FEB-1998; 98US-0075460P.

PR 19-FEB-1998; 98US-0075461P.

PR 19-FEB-1998; 98US-0075462P.

PR 19-FEB-1998; 98US-0075463P.

PR 19-FEB-1998; 98US-0075464P.

PR 06-MAR-1998; 98US-0076912P.

PR 09-MAR-1998; 98US-0077229P.

PR 09-MAR-1998; 98US-0077230P.

PR 09-MAR-1998; 98US-0077231P.

PR 18-MAR-1998; 98US-0080844P.

PR 07-APR-1998; 98US-0083067P.

PR 27-APR-1998; 98US-0083386P.

PR 29-APR-1998; 98US-0083387P.

PR 29-APR-1998; 98US-0083388P.

PR 29-APR-1998; 98US-0083390P.

PR 13-MAY-1998; 98US-0085222P.

PR 13-MAY-1998; 98US-0085223P.

PR 13-MAY-1998; 98US-0085224P.

PR 21-MAY-1998; 98US-0086183P.

PR 21-MAY-1998; 98US-0086184P.

PR 21-MAY-1998; 98US-0086185P.

PR 21-MAY-1998; 98US-0086186P.

PR 21-MAY-1998; 98US-0086187P.

PR 01-JUN-1998; 98US-0087422P.

PR 25-SEP-1998; 98US-0101707P.

PR 13-OCT-1998; 98US-0104123P.

PR 13-OCT-1998; 98US-0104124P.

PR 13-OCT-1998; 98US-0104126P.

PR 13-OCT-1998; 98US-0104127P.

PR 13-OCT-1998; 98US-0104128P.

PR 18-NOV-1998; 98US-0108996P.

PR 19-NOV-1998; 98US-0109018P.

PR 24-NOV-1998; 98US-00199129.

PR 08-DEC-1998; 98US-00210297.

PR 11-DEC-1998; 98US-0111981P.

PR 22-DEC-1998; 98US-0113224P.

PR 12-JAN-1999; 99US-00229413.

XX (CHEI/) CHEIKH N.

PA (FISH/) FISHER D K.

PA (LIU/) LIU J.

XX Cheikh N, Fisher DK, Liu J;

XX WPI; 2003-688722/65.

XX New maize or soybean enzymes and nucleic acid molecules associated with

PT the sucrose pathway, useful for genome mapping, gene identification and

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PT expression.

XX Claim 2; Page; 117pp; English.

PS The invention relates to a substantially purified nucleic acid molecule

CC (appearing as ADAS7847 - ADA60660 that encodes a maize or soybean enzyme

CC or its fragment, associated with the sucrose pathway selected from:

CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose

CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,

CC vacuolar hydrogen translocating pyrophosphatase, pyrophosphatase-dependent

CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,

CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,

CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine

CC diphosphate (UMP)-glucose pyrophosphorylase. Also included are a

CC substantially purified maize or soybean enzyme (or its fragment) and a

CC transformed plant having a nucleic acid molecule. Also disclosed as new

CC are purified antibodies capable of specifically binding to the maize or

CC soybean enzyme, determining a level or pattern of a plant sucrose pathway

CC enzyme in a plant cell or plant tissue, determining a mutation in a plant

CC whose presence is predictive of a mutation affecting the level or pattern

CC of a plant sucrose pathway enzyme, producing a plant containing an

CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing

CC expression of a plant sucrose pathway enzyme in a plant and determining

CC an association between a polymorphism and a plant trait. The maize or

CC soybean enzymes and nucleic acid molecules are useful for genome mapping,

CC gene identification and analysis, plant breeding, or preparation of

CC constructs for plant gene expression and transgenic plants. The nucleic

CC acid molecules are also useful as markers or probes. The present sequence

CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose

CC pathway enzyme. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX Sequence 150 BP; 39 A; 39 C; 29 G; 43 T; 0 U; 0 Other;

XX Query Match 5.5%; Score 150; DB 8; Length 150;

XX Best Local Similarity 100.0%; Pred. No. 3,7e-49;

XX Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1497 ACCGAGTTGTCNAGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCTGGAG 1556

DB 1 ACCGAGTTGTCNAGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCTGGAG 60

QY 1557 CTGACATGTCCATATATCTTCCACATACCGAGAGCCGAGCGACTCACCTCTCTTCATG 1616

DB 61 CTGACATGTCCATATATCTTCCACATACCGAGAGCCGAGCGACTCACCTCTCTTCATG 120

QY 1617 GTTCAATCGAAATTTGATTATGACCCGG 1646

Db 121 GTTCAATCGAAATTGATTATGACCGG 150

RESULT 11

ADA58864

ADA58864 standard; cDNA; 411 BP.

XX AC ADA58864;

XX DE

DT 20-NOV-2003 (first entry)

XX DE

XX DE Maize sucrose synthase EST #508.

XX KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;

XX KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;

XX KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;

XX KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;

XX KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;

XX KW invertase; sucrose synthase; hexokinase; fructokinase;

XX KW nucleoside diphosphate kinase-kinase; NDP;

XX KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;

XX KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX OS Zea mays.

XX PN US2003135870-A1.

XX PD 17-JUL-2003.

XX PF 26-JAN-1999; 99US-00237183.

XX PR 24-NOV-1997; 97US-0067000P.

XX PR 09-DEC-1997; 97US-0069472P.

XX PR 27-JAN-1998; 98US-0072888P.

XX PR 10-FEB-1998; 98US-0074201P.

XX PR 10-FEB-1998; 98US-0074280P.

XX PR 10-FEB-1998; 98US-0074281P.

XX PR 10-FEB-1998; 98US-0074282P.

XX PR 12-FEB-1998; 98US-0074555P.

XX PR 12-FEB-1998; 98US-0074566P.

XX PR 12-FEB-1998; 98US-0074567P.

XX PR 19-FEB-1998; 98US-0074789P.

XX PR 19-FEB-1998; 98US-0075459P.

XX PR 19-FEB-1998; 98US-0075460P.

XX PR 19-FEB-1998; 98US-0075461P.

XX PR 19-FEB-1998; 98US-0075462P.

XX PR 19-FEB-1998; 98US-0075463P.

XX PR 19-FEB-1998; 98US-0075464P.

XX PR 06-MAR-1998; 98US-0076912P.

XX PR 09-MAR-1998; 98US-0077239P.

XX PR 09-MAR-1998; 98US-0077230P.

XX PR 09-MAR-1998; 98US-0077231P.

XX PR 18-MAR-1998; 98US-0078368P.

XX PR 27-APR-1998; 98US-0080844P.

XX PR 27-APR-1998; 98US-0083067P.

XX PR 29-APR-1998; 98US-0083386P.

XX PR 29-APR-1998; 98US-0083387P.

XX PR 29-APR-1998; 98US-0083388P.

XX PR 29-APR-1998; 98US-0083389P.

XX PR 29-APR-1998; 98US-0083390P.

XX PR 13-MAY-1998; 98US-0085222P.

XX PR 13-MAY-1998; 98US-0085223P.

XX PR 13-MAY-1998; 98US-0085224P.

XX PR 21-MAY-1998; 98US-0086183P.

XX PR 21-MAY-1998; 98US-0086184P.

XX PR 21-MAY-1998; 98US-0086185P.

XX PR 21-MAY-1998; 98US-0086186P.

XX PR 21-MAY-1998; 98US-0086187P.

XX PR 21-MAY-1998; 98US-0086188P.

XX PR 01-JUN-1998; 98US-0087422P.

XX PR 16-JUN-1998; 98US-0089524P.

XX PR 18-JUN-1998; 98US-0089793P.

PR 18-JUN-1998; 98US-0089810P.

PR 18-JUN-1998; 98US-0089814P.

PR 22-JUN-1998; 98US-0090170P.

PR 26-JUN-1998; 98US-0090928P.

PR 29-JUN-1998; 98US-0091035P.

PR 30-JUN-1998; 98US-0091405P.

PR 08-JUL-1998; 98US-0092036P.

PR 09-SEP-1998; 98US-0095667P.

PR 09-SEP-1998; 98US-0095670P.

PR 09-SEP-1998; 98US-0095697P.

PR 16-SEP-1998; 98US-0100672P.

PR 16-SEP-1998; 98US-0100673P.

PR 16-SEP-1998; 98US-0100674P.

PR 21-SEP-1998; 98US-0101130P.

PR 21-SEP-1998; 98US-0101131P.

PR 21-SEP-1998; 98US-0101132P.

PR 22-SEP-1998; 98US-0101343P.

PR 22-SEP-1998; 98US-0101344P.

PR 22-SEP-1998; 98US-0101347P.

PR 22-SEP-1998; 98US-0101508P.

PR 25-SEP-1998; 98US-0101707P.

PR 13-OCT-1998; 98US-0104123P.

PR 13-OCT-1998; 98US-0104124P.

PR 13-OCT-1998; 98US-0104126P.

PR 13-OCT-1998; 98US-0104127P.

PR 18-NOV-1998; 98US-0104128P.

PR 19-NOV-1998; 98US-0109018P.

PR 24-NOV-1998; 98US-00199129.

PR 08-DEC-1998; 98US-00210297.

PR 11-DEC-1998; 98US-0111981P.

PR 22-DEC-1998; 98US-0113224P.

PR 12-JAN-1999; 99US-00229413.

XX (CHEI/) CHEIKH N.

PA (FISH/) FISHER D K.

PA (LIU/) LIU J.

XX Cheikh N, Fisher DK, Liu J;

XX WPI; 2003-688722/65.

PT New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression.

PT Claim 2; Page: 117pp; English.

PS The invention relates to a substantially purified nucleic acid molecule (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme or its fragment, associated with the sucrose pathway selected from: triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase, vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent fructose-6-phosphate phosphotransferase, invertase, sucrose synthase, hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase, glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine diphosphate (UDP)-glucose pyrophosphorylase. Also included are a substantially purified maize or soybean enzyme (or its fragment) and a transformed plant having a nucleic acid molecule. Also disclosed as new are purified antibodies capable of specifically binding to the maize or soybean enzyme, determining a level or pattern of a plant sucrose pathway enzyme in a plant cell or plant tissue, determining a mutation in a plant whose presence is predictive of a mutation affecting the level or pattern of a plant sucrose pathway enzyme, producing a plant containing an overexpressed or reduced level of plant sucrose pathway enzyme, reducing expression of a plant sucrose pathway enzyme in a plant and determining an association between a polymorphism and a plant trait. The maize or soybean enzymes and nucleic acid molecules are useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression and transgenic plants. The nucleic acid molecules are also useful as markers or probes. The present sequence

CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX SQ Sequence 411 BP; 99 A; 109 C; 113 G; 88 T; 0 U; 2 Other;

Query Match 5.2%; Score 143; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. NO. 1.9e-46;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1739 GGGCTGGTCCAGCTTTTCTAAGTGGCTTAAGCTGAGGGAGCTGTAACCTTGTGCTC 1798
DB 88 GGGCTGGTCCAGCTTTTCTAAGTGGCTTAAGCTGAGGGAGCTGTAACCTTGTGCTC 147
QY 1799 GTTCCGGGTACAATGATGTCACCAAGTCCAGGACAGGAGAGATCCGGAGATAGAG 1858
DB 148 GTTCCGGGTACAATGATGTCACCAAGTCCAGGACAGGAGAGATCCGGAGATAGAG 207
QY 1859 AAGATGCATGAATCATCAAGAC 1881
DB 208 AAGATGCATGAATCATCAAGAC 230

RESULT 12
ADA58374
ID ADA58374 standard; cDNA; 255 BP.
XX AC ADA58374;
XX JT 20-NCV-2003 (first entry)
XX DE Maize sucrose synthase EST #18.
XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucosyltransferase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX Zea mays.
XX OS
XX PN US2003135870-A1.
XX PD 17-JUL-2003.
XX PF 26-JAN-1999; 99US-00237183.
XX XX 24-NOV-1997; 97US-0067000P.
PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 10-FEB-1998; 98US-0074282P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 19-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
PR 19-FEB-1998; 98US-0075462P.
PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077229P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.

PR 18-MAR-1998; 98US-0078368P.
PR 07-APR-1998; 98US-0080844P.
PR 27-APR-1998; 98US-0083067P.
PR 29-APR-1998; 98US-0083386P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
PR 29-APR-1998; 98US-0083389P.
PR 29-APR-1998; 98US-0083390P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0093667P.
PR 09-SEP-1998; 98US-0096670P.
PR 09-SEP-1998; 98US-0096671P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.

(CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIU/) LIU J.

Cheikh N, Fisher DK, Liu J;
WPI; 2003-688722/45.

New maize or soybean enzymes and nucleic acid molecules associated with
the sucrose pathway, useful for genome mapping, gene identification and
analysis, plant breeding, or preparation of constructs for plant gene
expression.

Claim 2; Page; 117pp; English.

The invention relates to a substantially purified nucleic acid molecule
(appearing as ADA57847 - ADA60560 that encodes a maize or soybean enzyme
or its fragment, associated with the sucrose pathway selected from:
triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose

CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucosyltransferase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucosyltransferase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
 CC transformed plant having a nucleic acid molecule. Also disclosed as new
 CC are purified antibodies capable of specifically binding to the maize or
 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
 CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
 CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
 XX
 SQ Sequence 255 BP; 63 A; 62 C; 67 G; 63 T; 0 U; 0 Other;

Query Match 4.9%; Score 134; DB 8; Length 255;
 Best Local Similarity 100.0%; Pred. No. 7e-43;
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 564 ATGATAGAAATACAAAGCTTGGGGAGGCTTCACTCTGCTGACCAAAAGCTGAGGAGCACT 623
 Db |||||
 QY 624 TGTCAAAGCTCCCTGCTGACACACATCTCACAAATTTGCTTATAAATTTCAAGAGTGGG 683
 Db |||||
 QY 170 TGTCAAAGCTCCCTGCTGACACACATCTCACAAATTTGCTTATAAATTTCAAGAGTGGG 229
 Db |||||
 QY 684 GCGTGGAGAAAGGT 697
 Db 230 GCGTGGAGAAAGGT 243

RESULT 13
 ID ADA58370 standard; cDNA; 181 BP.
 AC ADA58370;
 DT 20-NOV-2003 (first entry)
 XX
 DE Maize sucrose synthase EST #14.
 XX
 KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
 KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucosyltransferase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucosyltransferase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.
 XX
 OS Zea mays.
 XX
 XX US2003135870-A1.
 XX
 XX 17-JUL-2003.
 PD
 XX
 PF 26-JAN-1999; 99US-00237183.
 XX
 XX 24-NOV-1997; 97US-0067000P.
 PR

PR 09-DEC-1997; 97US-0069472P.
 PR 27-JAN-1998; 98US-0072888P.
 PR 10-FEB-1998; 98US-0074201P.
 PR 10-FEB-1998; 98US-0074280P.
 PR 10-FEB-1998; 98US-0074281P.
 PR 12-FEB-1998; 98US-0074565P.
 PR 12-FEB-1998; 98US-0074566P.
 PR 12-FEB-1998; 98US-0074567P.
 PR 12-FEB-1998; 98US-0074789P.
 PR 19-FEB-1998; 98US-0075459P.
 PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
 PR 19-FEB-1998; 98US-0075462P.
 PR 19-FEB-1998; 98US-0075463P.
 PR 19-FEB-1998; 98US-0075464P.
 PR 06-MAR-1998; 98US-0076912P.
 PR 09-MAR-1998; 98US-0077229P.
 PR 09-MAR-1998; 98US-0077230P.
 PR 09-MAR-1998; 98US-0077231P.
 PR 18-MAR-1998; 98US-0078368P.
 PR 07-APR-1998; 98US-0080844P.
 PR 27-APR-1998; 98US-0083067P.
 PR 29-APR-1998; 98US-0083386P.
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 PR 21-MAY-1998; 98US-0086188P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
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 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
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 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210237.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.

Db 170 TGTCAGAGCTCCCTGCTGACACACCACTACTACACAAATTGCTTATATAATTTCTAGAGTGGG 229
QY 684 GC 685
Db 230 GC 231
RESULT 15
ADA58369 standard; cDNA; 310 BP.
XX AC ADA58369;
XX AC ADA58369;
DT 20-NOV-2003 (first entry)
XX DE Maize sucrose synthase EST #13.
XX KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX CS Zea mays.
XX PN US2003135870-A1.
XX PD 17-JUL-2003.
XX PF 26-JAN-1999; 99US-00237183.
XX PR 24-NOV-1997; 97US-0067000P.
PR 09-DEC-1997; 97US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 10-FEB-1998; 98US-0074382P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
PR 19-FEB-1998; 98US-0075462P.
PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077229P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.
PR 18-MAR-1998; 98US-0078366P.
PR 07-APR-1998; 98US-0080844P.
PR 27-APR-1998; 98US-0080867P.
PR 29-APR-1998; 98US-0083386P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
PR 29-APR-1998; 98US-0083389P.
PR 29-APR-1998; 98US-0083390P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.

PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0090170P.
PR 26-JUN-1998; 98US-0090928P.
PR 29-JUN-1998; 98US-0091035P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0099667P.
PR 09-SEP-1998; 98US-0099670P.
PR 09-SEP-1998; 98US-0099697P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
XX
PI Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX
DR New maize or soybean enzymes and nucleic acid molecules associated with
PT the sucrose pathway, useful for genome mapping, Gene identification and
PT analysis, plant breeding, or preparation of constructs for plant gene
PT expression.
XX
PS Claim 2; Page; 117pp; English.
XX
CC The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
CC or its fragment, associated with the sucrose pathway selected from:
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern
CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,

CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.
 XX
 SQ Sequence 310 BP; 89 A; 62 C; 64 G; 94 T; 0 U; 1 Other;

Query Match 4.2%; Score 114; DB 8; Length 310;
 Best Local Similarity 99.4%; Pred. No. 5.2e-35;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1364	CAGTTCACCTGCTGATATTAATGCTATGCAACGATGCTGATTTATCATCACCAGCACATAC	1423
DB	146	CAGTTCACCTGCTGATATTAATGCTATGCAACGATGCTGATTTATCATCACCAGCACATAC	205
QY	1424	CAAGAAATTCCTGGAAGCAAAATACCTGTTGGACAGTATGAGAGTCATATGCGCTTTACT	1483
DB	206	CAAGAAATTCCTGGAAGCAAAATACCTGTTGGACAGTATGAGAGTCATATGCGCTTTACT	265
QY	1484	CTGCCTGGTCTGTACCGAGTTGTCCATGGGATCGATGCTTCGAT	1528
DB	266	CTGCCTGGTCTGTACCGAGTTGTCCATGGGATCGATGCTTCGAT	310

Search completed: May 26, 2004, 02:50:33
 Job time : 691.979 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 01:50:08 ; Search time 4543.9 Seconds
(without alignments)

17987.372 Million cell updates/sec

Title: JS-10-080-114a-1

Perfect score: 2737

Sequence: 1 gtcacccacggtccggcg.....aaaaaaagggcgccgcg 2737

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 50

Total number of hits satisfying chosen parameters: 84

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmd.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_esti.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fua.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_pgk.*

27: em_gss_vrt.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1693	61.9	2705	11	AY104856 Zea mays
2	464	17.0	902	13	BQ619510 RESEQ1B02
3	351	12.8	411	12	BM500505 PAC000000
4	329	12.0	722	28	BZ322655 ia68b11.g

C	5	329	12.0	773	28	BZ316142
C	6	329	12.0	794	28	CC394967
C	7	329	12.0	813	29	CG069438
C	8	329	12.0	840	29	CC667244
C	9	329	12.0	982	29	CG069436
C	10	321	11.7	938	13	BQ619406
C	11	321	11.7	1005	13	BQ619258
C	12	317	11.6	662	28	BZ322987
C	13	313	11.4	313	14	CD984711
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C	15	312	11.4	316	14	CD984116
C	16	288	10.5	313	14	CD985046
C	17	287	10.5	435	12	BM500263
C	18	224	8.2	573	14	CF630867
C	19	224	8.2	645	28	BZ316481
C	20	217	7.9	731	29	CC733515
C	21	207	7.6	546	10	AW324745
C	22	200	7.3	690	14	CD442316
C	23	193	7.1	329	14	CD984266
C	24	158	5.8	315	29	CG275613
C	25	158	5.8	338	29	CG221855
C	26	158	5.8	499	10	BF728272
C	27	158	5.8	593	13	BUI02935
C	28	158	5.8	593	13	CA097247
C	29	158	5.8	648	29	CG377054
C	30	158	5.8	700	14	CA195492
C	31	158	5.8	835	14	CA280212
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C	33	157	5.7	908	29	CC628491
C	34	156	5.7	272	29	CG317557
C	35	156	5.7	445	29	CG659484
C	36	156	5.7	746	29	CG442293
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C	38	154	5.6	197	28	BZ543980
C	39	148	5.4	332	9	AI973432
C	40	147	5.4	188	28	BZ641703
C	41	146	5.3	804	28	BZ723706
C	42	144	5.3	324	14	CF637987
C	43	140	5.1	637	29	CC609870
C	44	136	5.0	815	29	CG004867
C	45	128	4.7	504	29	CG275601

ALIGNMENTS

RESULT 1	AY104856	Zea mays	2705 bp	mrna	linear	HTC 16-OCT-2002
LOCUS	AY104856	Zea mays	PCO079420	mrna	sequence.	
DEFINITION	AY104856	Zea mays	PCO079420	mrna	sequence.	
ACCESSION	AY104856	Zea mays	PCO079420	mrna	sequence.	
VERSION	AY104856.1	Zea mays	PCO079420	mrna	sequence.	
KEYWORDS	HTC.	Zea mays	PCO079420	mrna	sequence.	
SOURCE	HTC.	Zea mays	PCO079420	mrna	sequence.	
ORGANISM	HTC.	Zea mays	PCO079420	mrna	sequence.	
REFERENCE	1	(Bases 1 to 2705)				
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2	(Bases 1 to 2705)				
AUTHORS	CoE, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org ; ZmDB, www.zmdb.iastate.edu ; TIGR, www.tigr.org ; or NCBI, www.ncbi.nlm.nih.gov . When the source of the					

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.

FEATURES
source Location/Qualifiers

1..2705
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="maizeDB:634420"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/notes="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query March 61.9%; Score 1693; DB 11; Length 2705;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 18 GCGACCGGTGAGGACACCTCCACGCGCACCGCAACGAGCTCGTGGCCCTCTGTCCA 77
DB 1 GCGACCGGTGAGGACACCTCCACGCGCACCGCAACGAGCTCGTGGCCCTCTGTCCA 60

QY 78 AGTACGTGACAGGAGGAGGAGGATCTGAGCGCGCACCATCTCTGAGCGCTCGAAG 137
DB 61 AGTACGTGACAGGAGGAGGAGGATCTGAGCGCGCACCATCTCTGAGCGCTCGAAG 120

QY 138 AGGTCCAGGCTCCGCGGCGCGCTAGCTGAGGAGACCTTCCTCGAGCTCTCGCT 197
DB 121 AGGTCCAGGCTCCGCGGCGCGCTAGCTGAGGAGACCTTCCTCGAGCTCTCGCT 180

QY 198 CCGCGCAGAGGAGGAGCTGCTGCGCGCGGTTCGTGGCGATCGCGGTCCGCGCCCGG 257
DB 181 CCGCGCAGAGGAGGAGCTGCTGCTGCGCGGTTCGTGGCGATCGCGGTCCGCGCCCGG 240

QY 258 GAGTTGGAGTACGTCCGCGTCAAGGTTCCAGGAGCTCAGCGTCCAGGAGCTCAGAGTCT 317
DB 241 GAGTTGGAGTACGTCCGCGTCAAGGTTCCAGGAGCTCAGCGTCCAGGAGCTCAGAGTCT 300

QY 318 CCGAGTACCTCCGCTTCAAGGAGGAGCTTGTGACGCGCCAGGACCAATGATCCCTAGCTTC 377
DB 301 CCGAGTACCTCCGCTTCAAGGAGGAGCTTGTGACGCGCCAGGACCAATGATCCCTAGCTTC 360

QY 378 TCGAGCTTCACTTCGAGCGCTTCAGTCTCAGTCCCAAGCCCAATCGGTCAATCACTA 437
DB 361 TCGAGCTTCACTTCGAGCGCTTCAGTCTCAGTCCCAAGCCCAATCGGTCAATCACTA 420

QY 438 TTGGAAAAGGTGTGCAAGTTCCTCAACCGACACTTGTCTCAATCATGTTCCGCAACAGG 497
DB 421 TTGGAAAAGGTGTGCAAGTTCCTCAACCGACACTTGTCTCAATCATGTTCCGCAACAGG 480

QY 498 ATTGCTTGGAGCCCTGTGTGGATTTCTCGTGGCCACCGGACCAAGGGGCAATGATGA 557
DB 481 ATTGCTTGGAGCCCTGTGTGGATTTCTCGTGGCCACCGGACCAAGGGGCAATGATGA 540

QY 558 TCGTTAATGATGATACAAAGCTTGGGAGGCTTCAGTCTGCTGCTGACCAAGCTGAGG 617
DB 541 TCGTTAATGATGATACAAAGCTTGGGAGGCTTCAGTCTGCTGCTGACCAAGCTGAGG 600

QY 618 AGCACTTGTCAAGGCTCCCTGCTGACACACCATCTCAATTTGCTTATAATTTCAAG 677
DB 601 AGCACTTGTCAAGGCTCCCTGCTGACACACCATCTCAATTTGCTTATAATTTCAAG 660

QY 678 AGTGGGCTTGGAGAAAGGTGTGGGTGATACAGCAGGACATGTTTGGAAATGATCCATC 737
DB 661 AGTGGGCTTGGAGAAAGGTGTGGGTGATACAGCAGGACATGTTTGGAAATGATCCATC 720

QY 738 TCGTTCTAGACATCACTTAGGCGCCAGACCCATCTACCTTAGAGAAATTTCTGGGAGGA 797
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DB 781 TCCCATGATTTTAAAGCTTGTGTATATCCCTCATGAGNATCTTGGTCAAGCTAATG 840
QY 858 TATTAGGCTTCCAGACACAGGAGGACAGATCGTCTATATATCTGATCTGATCTGCGAC 917
DB 841 TATTAGGCTTCCAGACACAGGAGGACAGATCGTCTATATATCTGATCTGATCTGCGAC 900
QY 918 TAGAAATGATGTTCTCCGTTTAAAGAAAACAAGGCTTGTATTTTCCCAAGATTC 977
DB 901 TAGAAATGATGTTCTCCGTTTAAAGAAAACAAGGCTTGTATTTTCCCAAGATTC 960
QY 978 TCATTTGCTTCCGCTGATACACAGATCCAAAGGAAACATCATGCAATCAGCGCTGAGA 1037
DB 961 TCATTTGCTTCCGCTGATACACAGATCCAAAGGAAACATCATGCAATCAGCGCTGAGA 1020

QY 1038 GAATTTAGTGAACACAGCATACTTACATATTAAGAGTTCCCTTCAGAAATGAAATGGA 1097
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QY 1098 TACTTAAGAAATGGATATCAAGATTTGATGTGGCCATATCTGGAACAAATTTCTGAGG 1157
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QY 1158 ATGCTGCTGGTGAATTTGCTGCTGAATTAAGATTTCCAGACTTCAGACTTCATTAATGGA 1217
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QY 1278 ACATTCCTCATGCTCTGGAAGAAAGACTAAGTATCCAGATTCAGACATATTTTGAAGAA 1337
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DB 1381 CTGATTTTATCATCACAGCACATACAGAAATTTCTGGAAGCAAAATACTGTTGGAC 1440

QY 1458 AGTATGAGAGTCAATCTGCTTTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1517
DB 1441 AGTATGAGAGTCAATCTGCTTTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

QY 1518 ATGCTCTCGATCCAAAGTTCAATATAGTCTCTCTGAGGCTGACATGTCATATCTTTC 1577
DB 1501 ATGCTCTCGATCCAAAGTTCAATATAGTCTCTCTGAGGCTGACATGTCATATCTTTC 1560

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QY 1638 ATGACCCGAGGACAAAGATGAAACATTTGGGATCTGATGACCCGCTCAAGCCCATCC 1697
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DB 1741 CTAAGTCCCTAAGCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800

QY 1818 TCACAAGTCCAGGACAGGAGAGATCGCGAGATGAGAGATGAGATGATGATGATGATGATGAT 1877
DB 1801 TCACAAGTCCAGGACAGGAGAGATCGCGAGATGAGAGATGAGATGATGATGATGATGATGAT 1860

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Db 1861 AGACCCAGCACTGTTCCGGGAGTTCCGCTGCTCTCTGCCAGACAAACAGGGCCCGTA 1920
QY 1938 ACGGCGAGCTCTATCGCTACATCGCTGATACCCATGCTTTCGTCACAGCGGCGCTTGT 1997
Db 1921 ACGGCGAGCTCTATCGCTACATCGCTGATACCCATGCTTTCGTCACAGCGGCGCTTGT 1980
QY 1998 ATGAAGCGTTCCGCTCTACCGCTGTTGAGGCCATGACCTGTGGGCTTCCTACTTCGCGA 2057
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QY 2118 CGTACACACCCCAAGAGGCTGTTAATCTCATGSCCGACTTCTTCGACCGGTGCAAGCAAG 2177
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Db 2281 AGCTGTCGAGCTCGAGAGGCTGGAGAGCGGCTACCTTTCGAGATGTTCTTACATCTGA 2340
QY 2358 AGTTCGCGAGCTGCGAAGACCGTCCCGCTTGCATTCGAGATGTTCTTACATCTGA 2417
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Db 2461 GCGCGGAGCGGTAGCCCAATAAATGTGCCGAGCTGAACTGGTTTTT 2509

RESULT 2
BQ619510/c
LOCUS BQ619510
DEFINITION RESEQ1B02_SK.abl salt stressed Zea mays roots cDNA library Zea mays
cDNA clone RESEQ1B02_SK.abl similar to sucrose synthase [Zea mays],
mRNA sequence.
ACCESSION BQ619510
VERSION BQ619510.1 GI:21621504
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 902)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
1. .902
/organism="Zea mays"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3e-84;
Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 CTAGAGAAATCTTGGGGAGGATCCCATCAATTTTAAACGTTGTGTGGTATCCCTCAT 835
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QY 836 GGATACCTTTGGTCAAGCTAATGTTAGGCTTCCAGACACAGGAGCAGATCGTCTAT 895
Db 491 GGATACCTTTGGTCAAGCTAATGTTAGGCTTCCAGACACAGGAGCAGATCGTCTAT 432
QY 896 ATACTGGACCAAGTCCGTCACCTAGAAAATGAGATGTTCTCCGTTTAAAGAAAACAAGGG 955
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QY 956 CTTGATGTTTCCCAAGATTCATTTGTTACTCGGCTGATACAGATGCAAAAGGAACA 1015
Db 371 CTTGATGTTTCCCAAGATTCATTTGTTACTCGGCTGATACAGATGCAAAAGGAACA 312
QY 1016 TCATGCAATCAGCGCTTCGAGAAATAGTGAACACAGCATCTTACATATTACGAGTT 1075
Db 311 TCATGCAATCAGCGCTTCGAGAAATAGTGAACACAGCATCTTACATATTACGAGTT 252
QY 1076 CCCTTCAGAAAATGAAATGGGATACCTTAAAGAAATGGAATCAAGATTTGATGTGGCCA 1135
Db 251 CCCTTCAGAAAATGAAATGGGATACCTTAAAGAAATGGAATTTGATGTGGCCA 192
QY 1136 TATCTGGAACATTTCTGAGGATGCTGCTGGTGAATTCCTGCTGAATTAACAGGTACT 1195
Db 191 TATCTGGAACATTTCTGAGGATGCTGCTGGTGAATTCCTGCTGAATTAACAGGTACT 132
QY 1196 CCAGACTTCATATTGGAACACTACAGTATGGAATCTTGTGGC 1239
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RESULT 3

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BQ619510
LOCUS BQ619510
DEFINITION Pioneer AF-1 array Zea mays cDNA, mRNA sequence.
ACCESSION BQ619510
VERSION BQ619510.1 GI:18659754
KEYWORDS EST.
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SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 411)
Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
Jung, R.
```

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Maize opaque endosperm mutations create extensive changes in
patterns of gene expression
Unpublished (2002)
Contact: Jung R
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REFERENCE
AUTHORS Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
Jung, R.
TITLE Maize opaque endosperm mutations create extensive changes in
patterns of gene expression
JOURNAL Unpublished (2002)
COMMENT Contact: Jung R
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```
Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
Email: rudolf.jung@pioneer.com.
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FEATURES	source	Location/Qualifiers
ORIGIN		
Query Match		12.0%; Score 351; DB 12; Length 411;
Best Local Similarity		100.0%; P-ed. No. 2.5e-61;
Matches 351; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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Db	2	SCCTGTGCGACGGCAGCACAATGATCCCTACGTTCTCGAGCTTGCATTCGAGCGGTTCAA 61
QY	403	TGCTCTAGTCCCGACGCCCAATCGGTTCATCATCTATTTGGAAACGGTGTGAGTTCCTCAA 462
Db	62	TGCTCTAGTCCCGACGCCCAATCGGTTCATCATCTATTTGGAAACGGTGTGAGTTCCTCAA 121
QY	463	CCGACACTTGTCTCTCAATCATGTTCGCAACAGGGATTGCTTGGAGCCCTGTGGATTT 522
Db	122	CCGACACTTGTCTCTCAATCATGTTCGCAACAGGGATTGCTTGGAGCCCTGTGGATTT 181
QY	523	CCTCCGTGGCCACCGGCACAAAGGGCGATGTATGATGCTTAATGATAGATAACAAGCTT 582
Db	182	CCTCCGTGGCCACCGGCACAAAGGGCGATGTATGATGCTTAATGATAGATAACAAGCTT 241
QY	583	GGGGAGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCAGTGTGCAAGCTCCCTGCTGA 642
Db	242	GGGGAGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCAGTGTGCAAGCTCCCTGCTGA 301
QY	643	CACACCATACTCACAATTTGCTTATTAATTTCAAGAGTGGGGCTCGAGAA 693
Db	302	CACACCATACTCACAATTTGCTTATTAATTTCAAGAGTGGGGCTCGAGAA 352
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LOCUS		722 bp DNA linear GSS 06-NOV-2002
DEFINITION		ia68b11.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
ACCESSION		geomic clone ia68b11 5', genomic survey sequence.
VERSION		BZ322655
KEYWORDS		BZ322655.1 GI:24700292
SOURCE		GSS.
ORGANISM		Zea mays
REFERENCE		
AUTHORS		Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
TITLE		1 (bases 1 to 722);
JOURNAL		Rabinowicz, P.D., O'Shaughnessy, A.L., Ballia, V., Dedhia, N., Katzenburger, F., King, J., Miller, B., Muller, S., Nascimento, J., Zlatav, I., McCombie, W.R. and Martienssen, R.A.
COMMENT		Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)
		Contact: W. Richard McCombie
		Lita Annenberg Hazen Genome Sequencing Center
		Cold Spring Harbor Laboratory
		PO Box 100, Cold Spring Harbor, NY 11724, USA
		Tel: 516 367 8884
		Fax: 516 367 8874
		Email: mcombie@cshl.org
		Plate: ia68 row: b column: 11
		Seq primer: -21M13UnivRev
		Class: Shotgun
		High quality sequence stop: 722.
FEATURES		
source		Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.9e-57;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2371 GGCAGAACCGTGGCGCTTGCATTTGACCAACCCAGTAGCTTGGCAACTGCGAAGTGGCG 2430
Db 312 GGCAGAACCGTGGCGCTTGCATTTGACCAACCCAGTAGCTTGGCAACTGCGAAGTGGCG 371

Qy 2431 TAGCACTGGTACAAAGTGAACCTGAAGACCTTCAGTAATTTAGCGCGGCGAGACGG 2490
Db 372 TAGCACTGGTACAAAGTGAACCTGAAGACCTTCAGTAATTTAGCGCGGCGAGACGG 431

Qy 2491 TAGCCATAAATGTCGCGAGCTGAACCTGTTTTTATTATGACATAATGGCAGTATA 2550
Db 432 TAGCCATAAATGTCGCGAGCTGAACCTGTTTTTATTATGACATAATGGCAGTATA 491

Qy 2551 ACAAATTTACTGAAGGAGGTGGGTGTCAGTTGTGTGTTCTGTTACTGTATTAT 2610
Db 492 ACAATTTACTGAAGGAGGTGGGTGTCAGTTGTGTGTTCTGTTACTGTATTAT 551

Qy 2611 GTCAAGCTGTCGGTGCATTTCTTTGTCGCAAGCCGACGCACTGTGAAGTCTGAT 2670
Db 552 GTCAAGCTGTCGGTGCATTTCTTTGTCGCAAGCCGACGCACTGTGAAGTCTGAT 611

Qy 2671 AATACATCATATCTGTTGACCTGTGAA 2699
Db 612 AATACATCATATCTGTTGACCTGTGAA 640

RESULT 10

LOCUS B0619406 938 bp mRNA linear EST 06-SEP-2002
DEFINITION RNOSE07D02_SK.abl Salt stressed Zea mays roots cDNA library [Zea mays], mRNA sequence.

ACCESSION B0619406
VERSION B0619406.1 GI:21621400
KEYWORDS EST.

SOURCE

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 938)

REFERENCE
AUTHORS Wang, H. and Bohnert, H.J.
TITLE Genomics of plant stress tolerance
JOURNAL Unpublished (2002)

COMMENT Contact: Mark Fredrickson

Department of Plant Biology

University of Illinois

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 2172655473

Email: bohnertlab@life.uiuc.edu.

FEATURES

source

1..938
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
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Best Local Similarity 100.0%; Pred. No. 1.2e-55;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2198 ATATCTGGAGCAGGGCTGCAGCGCATATACGAGAAGTACACATGGAATATATCTACTCAGAG 2257
Db 418 ATATCTGGAGCAGGGCTGCAGCGCATATACGAGAAGTACACATGGAATATATCTACTCAGAG 477

Qy 2258 AGGTTGATGACATGCGCGGGGTCTACGGTTTCTGGAAGTACGTCTGAGCTCGAGAGG 2317
Db 478 AGGTTGATGACATGCGCGGGGTCTACGGTTTCTGGAAGTACGTCTGGAAGCTCGAGAGG 537

Qy 2318 CTGGAGACGAGCGCTACCTTGAGATGTTCTACATCTGGAAGTTCGCGAGCTGCGGAAG 2377
Db 538 CTGGAGACGAGCGCTACCTTGAGATGTTCTACATCTGGAAGTTCGCGAGCTGCGGAAG 597

Qy 2378 ACCGTGCGCGCTTGCAATTTGACCAACCGCAGTAGCTTGGCGCACTCGGACTGCGTAGCACT 2437
Db 598 ACCGTGCGCGCTTGCAATTTGACCAACCGCAGTAGCTTGGCGCACTCGGACTGCGTAGCACT 657

Qy 2438 TGGTACAGACCTGAAAACCTGAAAGACCTTCAGTAATTTAGGCGCGGCGAGACGGTAGCCAA 2497
Db 658 TGGTACAGACCTGAAAACCTGAAAGACCTTCAGTAATTTAGGCGCGGCGAGACGGTAGCCAA 717

Qy 2498 TAAATGTGCGGAGCTGAAC 2518
Db 718 TAAATGTGCGGAGCTGAAC 738

RESULT 11

LOCUS B0619258 1005 bp mRNA linear EST 06-SEP-2002
DEFINITION RNOSE05F01_SK.abl Salt stressed Zea mays roots cDNA library [Zea mays], mRNA sequence.

ACCESSION B0619258
VERSION B0619258.1 GI:21621252
KEYWORDS EST.

SOURCE

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1005)

REFERENCE Wang, H. and Bohnert, H.J.

Genomics of plant stress tolerance

Unpublished (2002)

Contact: Mark Fredrickson

Department of Plant Biology

University of Illinois

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 2172655473

Email: bohnertlab@life.uiuc.edu.

FEATURES

source

1..1005
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
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Query Match 11.7%; Score 321; DB 13; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.2e-55;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2198 ATATCTGGAGCAGGGCTGCAGCGCATATACGAGAAGTACACATGGAATATATCTACTCAGAG 2257
Db 418 ATATCTGGAGCAGGGCTGCAGCGCATATACGAGAAGTACACATGGAATATATCTACTCAGAG 477

Qy 2258 AGGTTGATGACATGCGCGGGGTCTACGGTTTCTGGAAGTACGTCTGAGCTCGAGAGG 2317

478	Db	AGGTTGATGACACTGGCGGGGCTCAGGTTTCTGGAAGTACTGTCTGGAAGCTCGAGAGG	537
2318	Qy	CTGGAGACGAGGCGCTACCTTTGAGATGTTTCTACATACTGAAGTTCCGCGAGCTGGCGAAG	2377
538	Db	CTGGAGACGAGGCGCTACCTTTGAGATGTTCTACATACTGAAGTTCCGCGAGCTGGCGAAG	597
2378	Qy	ACCGTGGCGCTTGCATTTGACCAACGCGAGTAGCTTCGCCAACTGCGACTGCGTAGCACT	2437
598	Db	ACCGTGGCGCTTGCATTTGACCAACCGAGTAGCTTCGCCAACTGCGACTGCGTAGCACT	657
2438	Qy	TGGTACAAGACTGAAACCTGAAGGACCTTCAGTAAATTTAGCGCGGCGAGACGGTAGCCAA	2497
658	Db	TGGTACAAGACTGAAACCTGAAGGACCTTCAGTAAATTTAGCGCGGCGAGACGGTAGCCAA	717
2498	Qy	TAAATGTGCCGAGCTGAAC	2518
718	Db	TAAATGTGCCGAGCTGAAC	738

RESULT 12					
BZ322987					
LOCUS	BZ322987	662 bp	DNA	linear	GSS 06-NOV-2002
DEFINITION	ia72f05.g1 WGS-ZmaysF (JM107 adapted methyl filtered)				Zea mays
	genomic clone ia72f05 5', genomic survey sequence.				

GSS.
Zea mays
Zea mays

KEYWORDS
SOURCE ORGANISM

Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 662)

AUTHORS
Rabiczewicz,P.D., O'Shaughnessy,A.L., Ballija,V., Dedhia,M.,
Katzemburger,F., King,L.B., Miller,B., Muller,S., Nascimento,L.,
Zutaern,T., McCombie,W.R. and Martienssen,R.A.,

TITLE
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)

C'OURNAL
CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: ia72 row: f column: 05
Seq primer: -21M13UnivRev
Class: Shotgun
High quality sequence stop: 662.

COMMENT

[illegible]

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FEATURES
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id=113
organism="Zea mays"
mol_type="RNA"
mol_title="r2"
db_xref="taxon:4577"
clone="QAM24f03"
issue_type="near leaf"
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Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1496 TACCGAGTTGTCATGGGTCGATGTCCTTCGATCGAAGTTCATATAGTCTCTCTCGGA 1555

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[illegible]

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Db      121  GGTTCATCGAAATTTGATTATGACCCGAGCAAAACGATGAACACATTTGGGCATCTG 180
Qy      1676  GATGACCGGTCAAGCCCACTCTTCTCCATGCGCAAGACTCGACAGGTCGAGAACATA 1735
Db      181  GATGACCGGTCAAGCCCACTCTTCTCCATGCGCAAGACTCGACAGGTCGAGAACATA 240
Qy      1736  ACAGGGCTGTCGAGCTTTTGTCTTAAGTCGGCTAAGCTGAGGAGCTGGTAAACCTTTGTC 1795
Db      241  ACAGGGCTGTCGAGCTTTTGTCTTAAGTCGGCTAAGCTGAGGAGCTGGTAAACCTTTGTC 300
Qy      1796  GTCGTTGCCGGGT 1808
Db      301  GTCGTTGCCGGGT 313

RESULT 14
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LOCUS   QAM24h06.yg QAM Zea mays cDNA clone QAM24h06, mRNA linear EST 16-JUL-2003
DEFINITION
ACCESSION CD984732
VERSION   CD984732.1 GI:32845051
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 :bases 1 to 313)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
            source
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ORIGIN
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Best Local Similarity 100.0%; Pred. No 1.3e-53;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1496  TACCGAGTTGTCATGGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCTGGA 1555
Db      1  TACCGAGTTGTCATGGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCTGGA 60
Qy      1556  GCTGACATGTCATATATCTTCCATACCGAGAGGCCAAGCGACTCCTCTCTTCAT 1615
Db      61  GCTGACATGTCATATATCTTCCATACCGAGAGGCCAAGCGACTCCTCTCTTCAT 120
Qy      1616  GGTTCATCGAAATTTGATTATGACCCGAGCAAAACGATGAACACATTTGGGCATCTG 1675
Db      121  GGTTCATCGAAATTTGATTATGACCCGAGCAAAACGATGAACACATTTGGGCATCTG 180
Qy      1676  GATGACCGGTCAAGCCCACTCTTCTCCATGCGCAAGACTCGACAGGTCGAGAACATA 1735
Db      181  GATGACCGGTCAAGCCCACTCTTCTCCATGCGCAAGACTCGACAGGTCGAGAACATA 240
Qy      1736  ACAGGGCTGTCGAGCTTTTGTCTTAAGTCGGCTAAGCTGAGGAGCTGGTAAACCTTTGTC 1795
Db      241  ACAGGGCTGTCGAGCTTTTGTCTTAAGTCGGCTAAGCTGAGGAGCTGGTAAACCTTTGTC 300

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Qy      1796  GTCGTTGCCGGGT 1808
Db      301  GTCGTTGCCGGGT 313

RESULT 15
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LOCUS   QAM17g10.yg QAM Zea mays cDNA clone QAM17g10, mRNA linear EST 16-JUL-2003
DEFINITION
ACCESSION CD984116
VERSION   CD984116.1 GI:32844435
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 :bases 1 to 316)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
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Qy      1557  CTGACATGTCATATATCTTCCATACCGAGAGGCCAAGCGACTCACCTCTCTTTCATG 1616
Db      65  CTGACATGTCATATATCTTCCATACCGAGAGGCCAAGCGACTCACCTCTCTTTCATG 124
Qy      1617  GTTCAATCGAAAATTTGATTTATGACCCGGAGCAAAACGATGAACACATTTGGGCATCTGG 1676
Db      125  GTTCAATCGAAAATTTGATTTATGACCCGGAGCAAAACGATGAACACATTTGGGCATCTGG 184
Qy      1677  ATGACCGGTCAAGCCCACTCTCTTCCATGCGCAAGACTCGACAGGTCGAGAACATAA 1736
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Qy      1737  CAGGGCTGTCGAGCTTTTGTCTTAAGTCGGCTAAGCTGAGGAGCTGGTAAACCTTTGTCG 1796
Db      245  CAGGGCTGTCGAGCTTTTGTCTTAAGTCGGCTAAGCTGAGGAGCTGGTAAACCTTTGTCG 304
Qy      1797  TCGTTGCCGGGT 1808
Db      305  TCGTTGCCGGGT 316

Search completed: May 26, 2004, 09:17:58
Job time : 4550.9 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:35:47 ; Search time 7060.61 seconds
(without alignments)
16924.423 Million cell updates/sec

Title: US-10-080-114a-11

Perfect score: 2757

Sequence: 1 atgtctgcccgagctgaa.....aaaaaaagggggcgccgc 2757

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 50

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_bcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2561	92.9	2710	8	AY059416	AY059416 Zea mays
2	1989	72.1	2837	8	AY124703	AY124703 Zea mays
c	3	192	7.0	297	6	AX756452 Sequence
c	4	191	6.9	258	6	AX756409 Sequence
5	122	4.4	265	6	AR246503	AR246503 Sequence
6	103	3.7	221	11	BV079817	BV079817 sc1180_p3
7	103	3.7	225	11	BV079815	BV079815 sc1180_p3
8	103	3.7	234	11	BV079813	BV079813 sc1180_p3
9	103	3.7	239	11	BV079812	BV079812 sc1180_p3
10	103	3.7	239	11	BV079814	BV079814 sc1180_p3
11	103	3.7	239	11	BV079819	BV079819 sc1180_p3
12	72	2.6	240	11	BV079818	BV079818 sc1180_p3
13	69	2.5	234	11	BV079820	BV079820 sc1180_p3
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Zea mays sucrose synthase mRNA, partial cds.
ACCESSION AY059416
VERSION AY059416.1 GI:16797784
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2710)
Carlson, S.J., Chourey, P.S., Helentjaris, T. and Datta, R.
Gene expression studies on developing kernels of maize sucrose
synthase (Susy) mutants show evidence for a third Susy gene
plant Mol. Biol. (2001) In press
2 (bases 1 to 2710)
Helentjaris, T.
Direct Submission
Submitted (10-OCT-2001) Agronomic Traits/T&T, Pioneer Hi-Bred,
7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA
FEATURES
Location/Qualifiers
1..2710
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CDS

Pred. No. is the number of results predicted by chance to have a

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GCCAGGAGCCCTTCCTGACGCTCTCCGCTCCGCGCAGAGCGCGATGCTGCGCGCG 246
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QY 307 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACTCCGCTTCAAGGAGGAGCTT 366
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QY 367 GTCGAGGCGCAGACAAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGGTTCAATGTC 426
Db 330 GTCGAGGCGCAGACAAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGGTTCAATGTC 389

QY 427 TCAGTCCCAACCCAAATCGGTATCATCTATTGGAAAGCGGTGTCAGTTCCTCAACCGA 486
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QY 487 CACTTGTCTCAATCATGTTCCGCAACAGGGATGCTTGGAGCCCTGTGTGGATTTCCTC 546
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QY 547 CGTGGCCACCGCACAAGGGGCAATGATGATGCTTAATGATGATGATGATGATGATGATG 606
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QY 607 AGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCACTGTGCAAGCTTCCTGCTGACACA 666
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QY 667 CCATATCTACAAATTTGCTTATAAATTTCAAGAGTGGGGCTTGAGAAAGGTTGGGGTGA 726
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QY 727 ACAGGAGGACATGTTTGAATGATGCTCTCTCTCTAGACATCATTCAGGCGCCAGAC 786
Db 690 ACAGGAGGACATGTTTGAATGATGCTCTCTCTCTAGACATCATTCAGGCGCCAGAC 749

QY 787 CCATCTACCTAGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGCTTGTGTGGTA 846
Db 750 CCATCTACCTAGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGCTTGTGTGGTA 809

QY 847 TCCCTCATGGAATCTTTGGTCAAGCTTAATGATATTAGGCTTGCACACACAGGAGACAG 906
Db 810 TCCCTCATGGAATCTTTGGTCAAGCTTAATGATATTAGGCTTGCACACACAGGAGACAG 869

QY 907 ATCGTCTATATCTGACCAAGTCCGTGCACTAGAAAATGAGATGTTCTCCGTTAAAG 966
Db 870 ATCGTCTATATCTGACCAAGTCCGTGCACTAGAAAATGAGATGTTCTCCGTTAAAG 929

QY 967 AAACAAGGGCTTCATGTTTCCCAAGATTTCTCAATGTTTACTCGGCTGATPACAGATGCA 1026
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LOCUS Zea mays sucrose synthase 3 mRNA, complete cds.
DEFINITION Zea mays sucrose synthase 3 mRNA, complete cds.
ACCESSION AY124703
VERSION AY124703.1 GI:22121989
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
1 (bases 1 to 2837)
Holtgraeve, D.L., Scholz, A., Altmann, B. and Winter, H.
maize
Complete coding sequence of a third sucrose synthase isoform in
maize

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2837)
Holtgraeve, D.L., Scholz, A., Altmann, B. and Winter, H.
AUTHORS Holtgraeve, D.L., Scholz, A., Altmann, B. and Winter, H.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) Biology, University of Osnabrueck, Barbara
Strasse 11, Osnabrueck 49076, Germany
FEATURES
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2831
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2239; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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LOCUS AX756452 297 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 1191 from Patent WO03000905.
ACCESSION AX756452
VERSION AX756452.1 GI:32168583
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, R.,
Glazebrook, J., Katagiri, F., Kreis, J., Provart, N. and Ricke, D.
TITLE Identification and characterization of plant genes
JOURNAL Patent: WO 03000905-A 1191 03-JUN-2003;
Syngenta Participations AG (CH)
FEATURES
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Best Local Similarity 99.6%; Pred. No. 1.4e-89;
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Db 3 CAT 1
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LOCUS AX756409 258 bp DNA linear PAT 24-JUN-2003
DEFINITION Sequence 1148 from Patent WO03000905.
ACCESSION AX756409
VERSION AX756409.1 GI:32268540
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
Glazebrook, J., Katagiri, F., Kreps, J., Provart, N. and Rieke, D.,
Identification and characterization of plant genes
Patent: WO 03000905-A 1148 03-JAN-2003;
SYNGENTA PARTICIPATIONS AG (CH)
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Db 238 CACGAGCTCAGGCTCGAGGAGCTCACAGTCTCGAGTACCTCCGCTTCAAGGAGGAGCTT 79
QY 367 GTCGACGGCCA 377
Db 78 GTCGACGGCCA 68
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AR246503
LOCUS AR246503 265 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1862 from patent US 6476212.
ACCESSION AR246503
VERSION AR246503.1 GI:27294377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 265)
AUTHORS Lalgudi, R.V., Ito, L.Y. and Sherman, B.K.
TITLE Polynucleotides and polypeptides derived from corn ear
JOURNAL Patent: US 6476212-A 1862 05-NOV-2002;
FEATURES
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site.
ACCESSION BV079817
VERSION BV079817.1 GI:37051474
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 221)
AUTHORS McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
TITLE MPZ-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCACTGCC
Protocol:
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Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
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Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
Buffer:
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RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
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 Db 179 TAGCACTTGGTACAGACTGAAACCTGAGGACCTTCAGTAAT 221

RESULT 7

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 ACCESSION BV079815
 VERSION BV079815.1 GI:37051472
 KEYWORDS STS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 225)
 McMillen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: GAGGCGTACCTTGAGATGTTCTA
 Primer B: ATTATCAGCACTTCACCACTGCC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase PS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 47 44 40 34 66 61 63 82 82 80 82 82
 87 81 85 81 77 76 81 84 80 73 73 88 90 90 82 70 70 73 85 81 90
 81 90 83 79 79 79 84 81 88 83 86 90 90 79 82 88 90 82 82 90 84
 83 79 81 81 81 74 83 83 82 8.
 Location/Qualifiers

FEATURES

source

1. .225
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="CML322"
 /db_xref="taxon:4577"
 /clone_lib="Zea mays CML322"

/dev_stage="seedling"
 /note="Organ: leaf; genomic DNA from inbred line"
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STS

ORIGIN

Query Match 3.7%; Score 103; DB 11; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.5e-42;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2391 GCGAAGACCGTGGCGCTTGCATTCACCAACGCGAGTAGCTTGGCAACTGCGACTGGC 2450
 Db 123 GCGAAGACCGTGGCGCTTGCATTCACCAACGCGAGTAGCTTGGCAACTGCGACTGGC 182
 QY 2451 TAGCACTTGGTACAGACTGAAACCTGAGGACCTTCAGTAAT 2493
 Db 183 TAGCACTTGGTACAGACTGAAACCTGAGGACCTTCAGTAAT 225

RESULT 8

BVC79813
 LOCUS sc1180_p3 CML333 Zea mays CML333 Zea mays STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION BV079813
 VERSION BV079813.1 GI:37051470
 KEYWORDS STS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 234)
 McMillen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
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 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: GAGGCGTACCTTGAGATGTTCTA
 Primer B: ATTATCAGCACTTCACCACTGCC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase PS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 37 44 40 29 29 29 42 42 44 77 73 60
 55 51 58 53 82 82 82 82 81 85 85 80 76 77 77 77 75 73 90
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 Location/Qualifiers

FEATURES

source

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 /db_xref="taxon:4577"

[illegible]

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 Best Local Similarity 100.0%; Pred. No. 3.6e-26;
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QY 2422 CCGCAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGG 2481
 |||||
 DB 169 CCGCAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGG 228
 |||||
 QY 2482 ACCTTCAGTAAT 2493
 |||||
 DB 229 ACCTTCAGTAAT 240

RESULT 13

BV079820 234 bp DNA linear STS 30-SEP-2003
 LOCUS sc1180_p3 Hp301 Zea mays STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION BV079820
 VERSION BV079820.1 GI:37051477
 KEYWORDS STS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 234)
 McMillen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)

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 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: GAGGCGCTACCTTGAGATGTTCTA
 Primer B: ATTATCAGCACTTCACAGTGCC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 52 66 62 61 67 65 61 61 61 69 71 73 63
 66 64 72 72 87 88 84 80 80 85 84 81 76 77 80 71 73 70 84
 79 79 79 78 87 81 85 90 81 85 83 77 72 69 69 77 77 75 85 80
 79 90 90 90 90 81 81 84 84 82 90 90 79 77 70 75.
 Location/Qualifiers

FEATURES

source

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 Best Local Similarity 100.0%; Pred. No. 1.4e-24;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2425 CAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGGACC 2484
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 DB 166 CAGTAGCTTGGCAACTGCGACTCGTAGCACTTGGTACAGACTGAACCTGAAGGACC 225
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 QY 2485 TTCAGTAAT 2493
 |||||
 DB 226 TTCAGTAAT 234

RESULT 14

BV079821 246 bp DNA linear STS 30-SEP-2003
 LOCUS sc1180_p3 CML247 Zea mays CML247 Zea mays STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION BV079821
 VERSION BV079821.1 GI:37051478
 KEYWORDS STS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 246)
 McMillen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)

Contact: Brandon S. Gaut
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 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: GAGGCGCTACCTTGAGATGTTCTA
 Primer B: ATTATCAGCACTTCACAGTGCC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 42 37 34 34 42 42 42 42 42 42 26 26
 26 37 35 34 34 52 50 61 82 73 78 71 71 77 82 79 66 58 58
 58 55 63 63 80 80 84 75 70 66 61 56 61 61 67 67 84 84 79 90 83
 81 87 77 81 81 79 82 82 87 77 82 90 82 82 84 79 77 77 83 81 71

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83 80 71 66 60.
FEATURES      Location/Qualifiers
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              /mol_type="genomic DNA"
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              /db_xref="taxon:4577"
              /clone_lib="Zea mays CML247"
              /dev_stage="seedling"
              /note="Organ: leaf; genomic DNA from inbred line"
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STS
ORIGIN

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Query Match      2.5%; Score 69; DB 11; Length 246;
Best Local Similarity 100.0%; Pred.No.1.4e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2425 CAGTAGCTTGGCGCAACTGGGACTGGCTAGCACTTGGTACAGACTGAACCTGAAGGACC 2484
      |||||
Db 178 CAGTAGCTTGGCGCAACTGGGACTGGCTAGCACTTGGTACAGACTGAACCTGAAGGACC 237
      |||||

QY 2485 TTCAGTAAT 2493
      |||||
Db 238 TTCAGTAAT 246
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Search completed: May 26, 2004, 06:45:32
Job time : 7063.61 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:31:02 ; Search time 695.021 Seconds
(without alignments)
16851.697 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

Sequence: 1 atgtctgccgaagctgaa.....aaaaaaagggcgccgc 2757

Scoring table: OLIGO_NTC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 50

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 29Jan04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001s: *
5: geneseqn2001bs: *
6: geneseqn2002s: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2757	100.0	2757	6	AAD45856 Corn Sus3
2	2571	93.3	2737	6	AAD45849 Corn suc
3	278	10.1	428	8	ADA58861 Maize suc
4	255	9.2	303	8	ADA58379 Maize suc
5	246	8.9	347	6	AAD45857 Sorghum p
6	209	7.6	283	8	ADA58372 Maize suc
7	192	7.0	297	9	ADC08886 Corn DNA
8	191	6.9	258	9	ADC08843 Corn DNA
9	159	5.8	285	8	ADA58359 Maize suc
10	158	5.7	297	8	ADA58362 Maize suc
11	150	5.4	150	8	ADA58373 Maize suc
12	143	5.2	411	8	ADA58864 Maize suc
13	134	4.9	255	8	ADA58374 Maize suc
14	130	4.7	181	8	ADA58370 Maize suc
15	122	4.4	265	7	ABX83402 Corn ear-
16	114	4.1	310	8	ADA58369 Maize suc
17	99	3.6	148	8	ADA58371 Maize suc
18	83	3.0	137	8	ADA58375 Maize suc
19	63	2.3	284	8	ADA58368 Maize suc

ALIGNMENTS

RESULT 1
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ID AAD45856 standard; DNA; 2757 BP.
XX
XX AAD45856;
XX AC
XX 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)
XX
XX
DE Corn Sus3-Sorghum EST chimeric DNA.
XX
XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KW cellulose; corn; Sus3; chimeric; gene; ds.
XX
XX Zea mays.
OS Sorghum propinquum.
OS Chimeric.
XX
XX
FH Key Location/Qualifiers
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FT /product= "Corn Sus3-Sorghum EST chimeric protein"
FT misc_feature 1..39
FT /tag= b
FT /note= "Sorghum propinquum EST DNA"
FT misc_feature 40..2757
FT /tag= c
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XX WO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG, Niu X;
PI
XX WPI: 2002-691625/74.
XX P-PSDB; AAE28502.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving
PT plant or grain strength.
XX
XX Claim 1; Page 116-119; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant.
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is Corn Sus3-Sorghum EST chimeric DNA. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
XX Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2757; DB 6; Length 2757;
XX Best Local Similarity 100.0%; Pred.No. 0;
XX Matches 2757; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 1 ATGTCTGCCCCGAAGCTGAACCGACGCGAGCATCCGGACCGCGTCGAGGACACCCCTC 60

Db 1 AAGTGTGCCCCGAGCTGAACCGCAACGCGAGCATCCGGGACCGGTTCGAGGACACCCCTC 60
QY 61 CACGGGCAACCGCAACGAGCTCGCTCGCCCTCCCTCTCAAGTACGTGACCAAGGGGAGGGC 120
Db 61 CACGGGCAACCGCAACGAGCTCGCTCGCCCTCCCTCTCAAGTACGTGACCAAGGGGAGGGC 120
QY 221 ATCTGTGAGCGGACCAATCTCTGACGCGGCTCGAGAGGTTCAGGGCTCCGGGGTCCGC 180
Db 121 ATCTGTGAGCGGACCAATCTCTGACGCGGCTCGAGAGGTTCAGGGCTCCGGGGTCCGC 180
QY 181 GGGCTGCGCGAGGACCCCTTCCTCGAGCTCCCTCGGCTCCGGCTCCGGCTCCGGCTCCGGCT 240
Db 181 GGGCTGCGCGAGGACCCCTTCCTCGAGCTCCCTCGGCTCCGGCTCCGGCTCCGGCTCCGGCT 240
QY 241 CCGCGCTTCGTGGCCATCGCGCTCGCGGCTCGCGGCTCGCGGCTCGCGGCTCGCGGCT 300
Db 241 CCGCGCTTCGTGGCCATCGCGCTCGCGGCTCGCGGCTCGCGGCTCGCGGCTCGCGGCT 300
QY 301 AACGTTCAAGAGCTCAGCGTTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGG 360
Db 301 AACGTTCAAGAGCTCAGCGTTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGG 360
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Db 361 GAGCTTGTGAGCGGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAG 420
QY 421 AATGTCTAGTCCGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTC 480
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Db 481 AACCGACATTCGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAG 540
QY 541 TTCTCTCGGTGGCCAGGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAGCTCAGAG 600
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Db 661 GACACACCATCTCAATTCGCTTCAATTCGCTTCAATTCGCTTCAATTCGCTTCAATTCG 720
QY 721 GGTGATACAGCAGGACATGTTTTGGAAATGATTCATTCATTCATTCATTCATTCATTC 780
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QY 781 CCAGACCCATCTACCCCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTTGTT 840
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Db 841 GTGGATCCCTCATGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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Db 901 GGCACAGATCGTCTATATCTGACCAAGTCCGTGCACTAGAGAAATGAGATGTTTCCCGT 960
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Db 1081 TACATATTAAGAGTTCCTTTCAGAAATGAAATGGGATACTTAAAGAAATGGATATCAAGA 1140
QY 1141 TTTGATGTGTGGCATACTCTGAAACATTTGCTGAGGATGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 TTTGATGTGTGGCATACTCTGAAACATTTGCTGAGGATGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 GAAATACAGAGTACTCCAGACTTCATAATTTGGAACCTACAGTATGATGAAATCTTGTGG 1260
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QY 1261 TCAATGCTACTTCTTACAGATGGGAATTAACAGTGCACATTTGCTCATGCTCTGGAAG 1320
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QY 1381 TSCCAGTTCACCTGCTGATATAATTTGCTATGAACAAATGCTGATTTTATCATCACAGCACA 1440
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 Db 2281 TTGATGACACTGGCGCGGGTCTACGGTTCTTGGAGTACGCTGCGAAGCTCGAGAGGCTG 2340
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 Db 2341 GAGACGAGGGCTACCTTGAGATGTTCTACATACCTGAAGTTCGCGAGCTGGGGAAGCC 2400
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 Db 2641 CGGCTGCAATTTCTTCTGCGAAGCGCGAGGCACTGCTGAAGTGTGCTGATAAATACATCA 2700
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 Db 2701 TATTTCTGTCACCTGTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGCGC 2757

RESULT 2
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 ID AAD45849 standard; cDNA; 2737 BP.
 XX
 AC AAD45849;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Corn sucrose synthase (Sus3) cDNA.
 XX
 KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 KW cellulose; corn; Sus3; gene; ss.
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 OS Zea mays.
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 FH Key Location/Qualifiers
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 XX WO200267662-A1.
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 PD 06-SEP-2002.
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 PF 21-FEB-2002; 2002MO-US005137.
 XX
 PR 22-FEB-2001; 2001US-0270777P.
 XX
 PA (PION-) PIONEER HZ-BRED INT INC.
 XX
 PI Dhugga KS, Helentjaris TG, Niu X;
 XX
 DR WPI; 2002-691625/74.
 DR P-PSDB; AAE28499.

XX New polynucleotide and its encoded sucrose synthase, useful for
 FT modulating the level of sucrose synthase in transgenic plants (e.g. maize
 FT or soybean) to improve stalk length, reduce grain breakage, or improving
 FT plant or grain strength.
 XX
 PS Claim 1; Page 102-103; 125pp; English.
 XX
 CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
 CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
 CC acids. The polynucleotide, or its encoded protein, is useful for
 CC modulating the level of sucrose synthase in a transgenic plant,
 CC increasing cellulose production in the stalk tissue of a transgenic
 CC plant, or increasing the concentration of cellulose in the tissues of a
 CC seed of a transgenic plant. This is particularly useful in plant (e.g. in
 CC maize or soybean) breeding, especially for e.g. improving stalk length in
 CC maize, reducing grain breakage during combining, transport or movement
 CC into storage, or improving plant or grain strength. The present sequence
 CC is corn Sus3 cDNA
 XX
 SQ Sequence 2737 BP; 711 A; 672 C; 697 G; 657 T; 0 U; 0 Other;
 Query Match 93.3%; Score 2571; DB 6; Length 2737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

ADA58861

ID ADA58861 standard; cDNA; 428 BP.

XX ADA58861;

AC AC

XX 20-NOV-2003 (first entry)

DT

XX Maize sucrose synthase EST #505.

DE

XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;

KM triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;

KM fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;

KM pyrophosphatase; vacuolar hydrogen translocating pyrophosphatase;

KM pyrophosphate-dependent fructose-6-phosphate phosphotransferase;

KM invertase; sucrose synthase; hexokinase; fructokinase;

KM nucleoside diphosphate kinase-kinase; NDP;

KM glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;

KM uridine diphosphate-glucose pyrophosphorylase; maize.

XX

OS Zea mays.
XX US2003-3587C-A1.
XX 17-JUL-2003.
XX 26-JAN-1999; 99US-00237183.
XX 24-NOV-1997; 97US-0067000P.
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XX 27-JAN-1998; 98US-0072888P.
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PR 18-NOV-1998; 98US-0108996P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 99US-00229413.
XX (CHEI/) CHEIKH N.
XX (FISH/) FISHER D K.
XX (LIU/) LIU J.
XX Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX New maize or soybean enzymes and nucleic acid molecules associated with
XX the sucrose pathway, useful for genome mapping, gene identification and
XX analysis, plant breeding, or preparation of constructs for plant gene
XX expression.
XX Claim 2; Page; 117pp; English.
XX The invention relates to a substantially purified nucleic acid molecule
XX (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
XX or its fragment, associated with the sucrose pathway selected from:
XX triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
XX 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
XX vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
XX fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
XX hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
XX glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine
XX diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
XX substantially purified maize or soybean enzyme (or its fragment) and a
XX transformed plant having a nucleic acid molecule. Also disclosed as new
XX are purified antibodies capable of specifically binding to the maize or
XX soybean enzyme, determining a level or pattern of a plant sucrose pathway
XX enzyme in a plant cell or plant tissue, determining a mutation in a plant
XX whose presence is predictive of a mutation affecting the level or pattern
XX of a plant sucrose pathway enzyme, producing a plant containing an
XX overexpressed or reduced level of plant sucrose pathway enzyme, reducing
XX expression of a plant sucrose pathway enzyme in a plant and determining
XX an association between a polymorphism and a plant trait, the maize or
XX soybean enzymes and nucleic acid molecules are useful for genome mapping,
XX gene identification and analysis, plant breeding, or preparation of
XX constructs for plant gene expression and transgenic plants. The nucleic
XX acid molecules are also useful as markers or probes. The present sequence
XX is a maize EST (expressed sequence tag) from a gene encoding a sucrose
XX pathway enzyme. Note: the sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
SQ Sequence 428 BP; 118 A; 95 C; 126 G; 89 T; 0 U; 0 Other;
Query Match 10.1%; Score 278; DB 8; Length 428;
Best Local Similarity 99.7%; Pred. No. 1.1e-99;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 4
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AC ADA58379;
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XX 20-NOV-2003 (first entry)
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XX Maize sucrose synthase EST #23.
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XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
XX triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
XX fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
XX pyrophosphatase; vacuolar hydrogen translocating-pyrophosphatase;
XX pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
XX invertase; sucrose synthase; hexokinase; fructokinase;
XX nucleoside diphosphate kinase-kinase; NDP;
XX glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
XX uridine diphosphate-glucose pyrophosphorylase; maize.
XX
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XX
XX US2003:3587C-A1.
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XX 17-JUL-2003.
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PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089793P.
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PR 22-SEP-1998; 98US-0101344P.
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PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
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PR 18-NOV-1998; 98US-0108969P.
PR 19-NOV-1998; 98US-0109018P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
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PR 12-JAN-1999; 98US-00229413.
XX
XX (CHRI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
PI
XX Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/45.
XX
XX New maize or soybean enzymes and nucleic acid molecules associated with
XX the sucrose pathway, useful for genome mapping, gene identification and
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XX expression.
XX
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XX (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
XX or its fragment, associated with the sucrose pathway selected from:
XX triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
XX 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose-6-phosphate
XX vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
XX hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
XX glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine
XX diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
XX substantially purified maize or soybean enzyme (or its fragment) and a
XX transformed plant having a nucleic acid molecule. Also disclosed as new
XX are purified antibodies capable of specifically binding to the maize or
XX soybean enzyme, determining a level or pattern of a plant sucrose pathway
XX enzyme in a plant cell or plant tissue, determining a mutation in a plant
XX whose presence is predictive of a mutation affecting the level or pattern

```

CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.
XX
SQ Sequence 303 BP; 71 A; 78 C; 86 G; 68 T; 0 U; 0 Other;

Query Match 9.2%; Score 255; DB 8; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1761 GCTGTCGAGCTTTTGTAAAGTCGCTAAGCTGAGGAGCTGTAAACCTTGTGTCGT 1820
DB 1 GCTGTGAGAGCTTTTGTAAAGTCGCTAAGCTGAGGAGCTGTAAACCTTGTGTCGT 60
QY 1821 TGCCGGGTACAATGATGTCAACAGTCCAGGACAGGGAAGAGATCGCGAGATAGAGAA 1880
DB 61 TGCCGGGTACAATGATGTCAACAGTCCAGGACAGGGAAGAGATCGCGAGATAGAGAA 120
QY 1881 GATGTCATGAATCATCAGACCCCACTTTTTCGGGAGTTCGCTGGATCTCTGCCCA 1940
DB 121 GATGTCATGAATCATCAGACCCCACTTTTTCGGGAGTTCGCTGGATCTCTGCCCA 180
QY 1941 GACAAACAGGCGCCGTAAACGGCGAGCTCTATCGCTACATCGCTGATCCCATGTGCTTT 2000
DB 181 GACAAACAGGCGCCGTAAACGGCGAGCTCTATCGCTACATCGCTGATCCCATGTGCTTT 240
QY 2001 CGTACAGCCGCGCTT 2015
DB 241 CGTACAGCCGCGCTT 255

RESULT 5
AAD45857
ID AAD45857 standard; DNA; 347 BP.
XX
AC AAD45857;
XX
DT 27-DEC-2002 (first entry)
XX
DE Sorghum propinquum EST DNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sush1;
KW transgenic plant; plant breeding; grain breakage; grain strength; EST;
KW cellulose; gene; ds.
XX
OS Sorghum propinquum.
XX
PN W0200267662-A1.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005137.
XX
PR 22-FEB-2001; 2001US-0270777P.
XX
PA (PION-) PIONEER HI-BRED INT' INC.
XX
PI Dhugga KS, Helentjaris TG, Niu X;
XX
DR WPI; 2002-691625/74.
XX
PT New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving

PT plant or grain strength.
XX
XX Example 11; Page 121; 125pp; English.
XX
CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
CC constitutive sucrose synthase (Sush1) and their corresponding nucleic
CC acids. The polynucleotide, or its encoded protein, is useful for
CC modulating the level of sucrose synthase in a transgenic plant,
CC increasing cellulose production in the stalk tissue of a transgenic
CC plant, or increasing the concentration of cellulose in the tissues of a
CC seed of a transgenic plant. This is particularly useful in plant (e.g.
CC maize or soybean) breeding, especially for e.g. improving stalk length in
CC maize, reducing grain breakage during combining, transport or movement
CC into storage, or improving plant or grain strength. The present sequence
CC is Sorghum propinquum EST DNA used in the exemplification of the
CC invention
XX
SQ Sequence 347 BP; 60 A; 141 C; 109 G; 37 T; 0 U; 0 Other;

Query Match 8.9%; Score 246; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 4.8e-87;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCTGCTCCCGAAGCTCAACCGCAACCGAGCATCCGGGACCGGTCGAGGACACCTTC 60
DB 102 ATGTCTGCTCCCGAAGCTCAACCGCAACCGAGCATCCGGGACCGGTCGAGGACACCTTC 161
QY 61 CACGGGACCCGCAAGAGCTGTGCTCTCTTCCAAAGTACGTGAACAGGGGAGGGC 120
DB 162 CACGGGACCCGCAAGAGCTGTGCTCTCTTCCAAAGTACGTGAACAGGGGAGGGC 221
QY 121 ATCTCTGAGCGCGACCATCATCTCGACGCGCTCGACGAGTCCAGGGTCCGGGTTCGC 180
DB 222 ATCTCTGAGCGCGACCATCATCTCGACGCGCTCGACGAGTCCAGGGTCCGGGTTCGC 281
QY 181 GCGCTCGCGCGAGGAGCCCTTCTCTGACGCTCTCTGACGCTCTCGCTCCGCGCAGGAGCGATCGTGTG 240
DB 282 GCGCTCGCGCGAGGAGCCCTTCTCTGACGCTCTCTGACGCTCTCGCTCCGCGCAGGAGCGATCGTGTG 341
QY 241 CCGCGC 246
DB 342 CCGCGC 347

RESULT 6
ADA58372
ID ADA58372 standard; cDNA; 283 BP.
XX
AC ADA58372;
XX
DT 20-NOV-2003 (first entry)
XX
DE Maize sucrose synthase EST #16.
XX
KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
KW pyrophosphatase; vacuolar hydrogen translocating-pyrophosphatase;
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
KW invertase; sucrose synthase; hexokinase; fructokinase;
KW nucleoside diphosphate kinase-kinase; NDP;
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
KW uridine diphosphate-glucose pyrophosphorylase; maize.
XX
OS Zea mays.
XX
PN US2003135870-A1.
XX
PD 17-JUL-2003.
XX
PF 26-JAN-1999; 99US-00237183.
XX
PR 24-NOV-1997; 97US-0067000P.

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PR 09-DEC-1997; 98US-0069472P.
PR 27-JAN-1998; 98US-0072888P.
PR 10-FEB-1998; 98US-0074201P.
PR 10-FEB-1998; 98US-0074280P.
PR 10-FEB-1998; 98US-0074281P.
PR 10-FEB-1998; 98US-0074282P.
PR 12-FEB-1998; 98US-0074565P.
PR 12-FEB-1998; 98US-0074566P.
PR 12-FEB-1998; 98US-0074567P.
PR 19-FEB-1998; 98US-0074789P.
PR 19-FEB-1998; 98US-0075459P.
PR 19-FEB-1998; 98US-0075460P.
PR 19-FEB-1998; 98US-0075461P.
PR 19-FEB-1998; 98US-0075462P.
PR 19-FEB-1998; 98US-0075463P.
PR 19-FEB-1998; 98US-0075464P.
PR 06-MAR-1998; 98US-0076912P.
PR 09-MAR-1998; 98US-0077229P.
PR 09-MAR-1998; 98US-0077230P.
PR 09-MAR-1998; 98US-0077231P.
PR 18-MAR-1998; 98US-0078368P.
PR 07-APR-1998; 98US-0080844P.
PR 27-APR-1998; 98US-0083067P.
PR 29-APR-1998; 98US-0083387P.
PR 29-APR-1998; 98US-0083388P.
PR 29-APR-1998; 98US-0083389P.
PR 29-APR-1998; 98US-0083390P.
PR 13-MAY-1998; 98US-0085222P.
PR 13-MAY-1998; 98US-0085223P.
PR 13-MAY-1998; 98US-0085224P.
PR 21-MAY-1998; 98US-0086183P.
PR 21-MAY-1998; 98US-0086184P.
PR 21-MAY-1998; 98US-0086185P.
PR 21-MAY-1998; 98US-0086186P.
PR 21-MAY-1998; 98US-0086187P.
PR 21-MAY-1998; 98US-0086188P.
PR 01-JUN-1998; 98US-0087422P.
PR 16-JUN-1998; 98US-0089524P.
PR 18-JUN-1998; 98US-0089733P.
PR 18-JUN-1998; 98US-0089810P.
PR 18-JUN-1998; 98US-0089814P.
PR 22-JUN-1998; 98US-0093170P.
PR 26-JUN-1998; 98US-0093928P.
PR 29-JUN-1998; 98US-0091535P.
PR 30-JUN-1998; 98US-0091405P.
PR 08-JUL-1998; 98US-0092036P.
PR 09-SEP-1998; 98US-0099667P.
PR 09-SEP-1998; 98US-0099670P.
PR 09-SEP-1998; 98US-0099672P.
PR 16-SEP-1998; 98US-0100672P.
PR 16-SEP-1998; 98US-0100673P.
PR 16-SEP-1998; 98US-0100674P.
PR 21-SEP-1998; 98US-0101130P.
PR 21-SEP-1998; 98US-0101131P.
PR 21-SEP-1998; 98US-0101132P.
PR 22-SEP-1998; 98US-0101343P.
PR 22-SEP-1998; 98US-0101344P.
PR 22-SEP-1998; 98US-0101347P.
PR 22-SEP-1998; 98US-0101508P.
PR 25-SEP-1998; 98US-0101707P.
PR 13-OCT-1998; 98US-0104123P.
PR 13-OCT-1998; 98US-0104124P.
PR 13-OCT-1998; 98US-0104126P.
PR 13-OCT-1998; 98US-0104127P.
PR 13-OCT-1998; 98US-0104128P.
PR 18-NOV-1998; 98US-0108996P.
PR 18-NOV-1998; 98US-0109015P.
PR 24-NOV-1998; 98US-00199129.
PR 08-DEC-1998; 98US-00210297.
PR 11-DEC-1998; 98US-0111981P.
PR 22-DEC-1998; 98US-0113224P.
PR 12-JAN-1999; 98US-00229413.

XX (CHEL/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
XX
XX Cheikh N, Fisher DK, Liu J;
XX WPI; 2003-688722/65.
XX
XX New maize or soybean enzymes and nucleic acid molecules associated with
PT the sucrose pathway, useful for genome mapping, gene identification and
PT analysis, plant breeding, or preparation of constructs for plant gene
XX expression.
XX
XX Claim 2; Page; 117pp; English.
XX
CC The invention relates to a substantially purified nucleic acid molecule
CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
CC or its fragment, associated with the sucrose pathway selected from:
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucosomerase,
CC vacuolar hydrogen translocating-phosphatase, pyrophosphate-dependent
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
CC substantially purified maize or soybean enzyme (or its fragment) and a
CC transformed plant having a nucleic acid molecule. Also disclosed as new
CC are purified antibodies capable of specifically binding to the maize or
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
CC whose presence is predictive of a mutation affecting the level or pattern
CC of a plant sucrose pathway enzyme, producing a plant containing an
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
CC expression of a plant sucrose pathway enzyme in a plant and determining
CC an association between a polymorphism and a plant trait. The maize or
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
CC gene identification and analysis, plant breeding, or preparation of
CC constructs for plant gene expression and transgenic plants. The nucleic
CC acid molecules are also useful as markers or probes. The present sequence
CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
CC pathway enzyme. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
XX
SQ Sequence 283 BP; 75 A; 74 C; 67 G; 67 T; 0 U; 0 Other;

Query Match 7.6%; Score 209; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.9e-72;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 CCAAGTTCATATAGTCTCTCTCTGGAGCTGACATGTCATATCTTCCACATACCGAG 1608
Db |||||
QY 1609 AAGGCCAAGCGACTCACCTCTCTTCATGGTTCAATCGAAATTTGATTTATGACCGGAG 1668
Db |||||
QY 1669 CAAAACGATGAACACATTTGGGCAATCTGGATGACCGGTCAAGCCCATCTCTTCTTCATG 1728
Db |||||
QY 1729 GCAAGACTCGACAGGGTGAAGACATAAC 1757
Db |||||
AD C08886/c
ID ADC08886 standarC; DNA; 297 BP.
XX
AC ADC08886;
```


XX DT 18-DEC-2003 (first entry)
 XX DE Corn DNA sequence Seq ID1191 related to grain filling.
 XX KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 XX KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX OS Zea mays.
 XX AC WO200300905-A2.
 XX PN 03-JAN-2003.
 XX DE 21-JUN-2002; 2002WO-IB002450.
 XX KW 22-JUN-2001; 2001US-0300112P.
 XX PR 26-SEP-2001; 2001US-0325277P.
 XX PR 20-DEC-2001; 2001US-0342327P.
 XX PA (SYN) SYNGENTA PARTICIPATIONS AG.
 XX PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX DR WPI; 2003-229341/22.
 XX PT New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX PS Disclosure; SEQ ID NO 1191; 130pp; English.
 XX CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence from corn which showed homology to rice "grain filling"
 CC genes of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.
 XX Sequence 297 BP; 87 A; 57 C; 70 G; 83 T; 0 U; 0 Other;
 XX
 XX Query Match 7.0%; Score 192; DB 9; Length 297;
 XX Best Local Similarity 99.6%; Pred. No. 3.6e-66;
 XX Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1393 GCTGATATATTCCTATGACATGCTGATTTATCATCCACGACATACCAAGAAATT 1452
 Db 243 GCTGATATATTCCTATGACATGCTGATTTATCATCCACGACATACCAAGAAATC 184
 QY 1453 GCTGGAAGCAAAAATCTGTTGACAGTATGAGATCATCTGCTTTACTCTGCTGCT 1512
 Db 183 GCTGGAAGCAAAAATCTGTTGACAGTATGAGATCATCTGCTTTACTCTGCTGCT 124
 QY 1513 CTGTACCGAGTTGCTTCATGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCCT 1572
 Db 123 CTGTACCGAGTTGCTTCATGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCCT 64
 QY 1573 GGAGCTGACATGTCATATATCTTCCATACACGAGAGCCCAAGGACATCACTCTCTTT 1632
 Db 63 GGAGCTGACATGTCATATATCTTCCATACACGAGAGCCCAAGGACATCACTCTCTTT 4

QY 1633 CAT 1635
 Db 3 CAT 1
 RESULT 8
 ADC08843/c
 ID ADC08843 standard; DNA; 258 BP.
 XX AC ADC08843;
 XX DT 18-DEC-2003 (first entry)
 XX DE Corn DNA sequence Seq ID1148 related to grain filling.
 XX KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 XX KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX OS Zea mays.
 XX AC WO200300905-A2.
 XX PN 03-JAN-2003.
 XX DE 21-JUN-2002; 2002WO-IB002450.
 XX KW 22-JUN-2001; 2001US-0300112P.
 XX PR 26-SEP-2001; 2001US-0325277P.
 XX PR 20-DEC-2001; 2001US-0342327P.
 XX PA (SYN) SYNGENTA PARTICIPATIONS AG.
 XX PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX DR WPI; 2003-229341/22.
 XX PT New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX PS Disclosure; SEQ ID NO 1148; 130pp; English.
 XX CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence from corn which showed homology to rice "grain filling"
 CC genes of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.
 XX Sequence 258 BP; 51 A; 87 C; 75 G; 45 T; 0 U; 0 Other;
 XX
 XX Query Match 6.9%; Score 191; DB 9; Length 258;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-65;
 XX Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 187 GCGAGGAGCCCTTCCTCGACGCTCTCGCTCCGCGCAGGAGCGATCGTCTGCCCGCG 246
 Db 258 GCGAGGAGCCCTTCCTCGACGCTCTCGCTCCGCGCAGGAGCGATCGTCTGCCCGCG 199

QY 247 TTCTGGCCATCGCGTGGCCGCGCGCGGAGTTTGGAGTACGTCGCGTCAACGTT 306
 Db 198 TTCTGGCCATCGCGTGGCCGCGCGCGGAGTTTGGAGTACGTCGCGTCAACGTT 139
 QY 307 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGAGTACCTCGCTTCAAGGAGGAGCTT 366
 Db 138 CACGAGCTCAGCGTCGAGCAGCTCACAGTCTCGAGTACCTCGCTTCAAGGAGGAGCTT 79
 QY 367 GTGACGGCCA 377
 Db 78 GTGACGGCCA 68

RESULT 9
 ADA58359
 ID ADA58359 standard; cDNA; 285 BP.
 XX
 AC ADA58359;
 XX
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Maize sucrose synthase EST #3.
 XX
 KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
 KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-Kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucose mutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.
 XX
 OS Zea mays.
 XX
 PN US2003135870-A1.
 XX
 PD 17-JUL-2003.
 XX
 XX 26-JAN-1999; 99US-00237183.
 XX
 PR 24-NOV-1997; 97US-0067000P.
 PR 09-DEC-1997; 97US-0069472P.
 PR 27-JAN-1998; 98US-0072888P.
 PR 10-FEB-1998; 98US-0074201P.
 PR 10-FEB-1998; 98US-0074280P.
 PR 10-FEB-1998; 98US-0074281P.
 PR 10-FEB-1998; 98US-0074282P.
 PR 12-FEB-1998; 98US-0074565P.
 PR 12-FEB-1998; 98US-0074566P.
 PR 12-FEB-1998; 98US-0074567P.
 PR 19-FEB-1998; 98US-0074789P.
 PR 19-FEB-1998; 98US-0075459P.
 PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
 PR 19-FEB-1998; 98US-0075462P.
 PR 19-FEB-1998; 98US-0075463P.
 PR 19-FEB-1998; 98US-0075464P.
 PR 06-MAR-1998; 98US-0076912P.
 PR 09-MAR-1998; 98US-0077229P.
 PR 09-MAR-1998; 98US-0077230P.
 PR 09-MAR-1998; 98US-0077231P.
 PR 18-MAR-1998; 98US-0078368P.
 PR 07-APR-1998; 98US-0080844P.
 PR 27-APR-1998; 98US-0083067P.
 PR 29-APR-1998; 98US-0083386P.
 PR 29-APR-1998; 98US-0083387P.
 PR 29-APR-1998; 98US-0083388P.
 PR 29-APR-1998; 98US-0083389P.
 PR 29-APR-1998; 98US-0083390P.
 PR 13-MAY-1998; 98US-0085222P.
 PR 13-MAY-1998; 98US-0085223P.
 PR 13-MAY-1998; 98US-0085224P.

PR 21-MAY-1998; 98US-0086183P.
 PR 21-MAY-1998; 98US-0086184P.
 PR 21-MAY-1998; 98US-0086185P.
 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089810P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
 PR 09-SEP-1998; 98US-0099667P.
 PR 09-SEP-1998; 98US-0099670P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
 PR 21-SEP-1998; 98US-0101132P.
 PR 22-SEP-1998; 98US-0101133P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.

(CHEI/) CHEIKH N.
 (FISH/) FISHER D K.
 (LIU/) LIU J.

Cheikh N, Fisher DK, Liu J;
 WPI; 2003-688722/45.

New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression.

Claim 2; Page; 117pp; English.

The invention relates to a substantially purified nucleic acid molecule (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme or its fragment, associated with the sucrose pathway selected from: triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase, vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent fructose-6-phosphate phosphotransferase, invertase, sucrose synthase, hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase, glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine diphosphate (UDP)-glucose pyrophosphorylase. Also included are a substantially purified maize or soybean enzyme (or its fragment) and a transformed plant having a nucleic acid molecule. Also disclosed as new are purified antibodies capable of specifically binding to the maize or soybean enzyme, determining a level or pattern of a plant sucrose pathway enzyme in a plant cell or plant tissue, determining a mutation in a plant

CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030135870.
 XX
 SQ Sequence 285 BP; 64 A; 82 C; 76 G; 63 T; 0 U; 0 Other;

Query Match 5.8%; Score 159; DB 8; Length 285;
 Best Local Similarity 100.0%; Pred. No. 9.9e-53;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1857 GGAAGAGATCGCGAGATAGAGAGATCGATGACTCATCAAGACCCCAACTTGTTCGG 1916
 Db 1 GGAAGAGATCGCGAGATAGAGAGATCGATGACTCATCAAGACCCCAACTTGTTCGG 60
 QY 1917 GCAGTTCCGCTGGATCTCTGCCAGACAAACAGGCGCGTAACCGCGAGCTCTATCGCTA 1976
 Db 61 GCAGTTCCGCTGGATCTCTGCCAGACAAACAGGCGCGTAACCGCGAGCTCTATCGCTA 120
 QY 1977 CATCGCTGATACCATGGTGTCTTCGTACACCGCGCCTT 2015
 Db 121 CATCGCTGATACCATGGTGTCTTCGTACACCGCGCCTT 159

RESULT 10

ADA58362

ID ADA58362 standard; cDNA; 297 BP.

XX AC ADA58362;

XX AC ADA58362;

DT 20-NOV-2003 (first entry)

XX DE Maize sucrose synthase EST #6.

XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;
 KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX OS Zea mays.

XX US2003135870-A1.

PD 17-JUL-2003.

XX PF 26-JAN-1999; 99US-00237163.

XX 24-NOV-1997; 97US-0067000P.

PR 09-DEC-1997; 97US-0069472P.

PR 27-JAN-1998; 98US-0072888P.

PR 10-FEB-1998; 98US-0074201P.

PR 10-FEB-1998; 98US-0074280P.

PR 10-FEB-1998; 98US-0074281P.

PR 10-FEB-1998; 98US-0074282P.

PR 12-FEB-1998; 98US-0074565P.

PR 12-FEB-1998; 98US-0074566P.

PR 12-FEB-1998; 98US-0074567P.

PR 19-FEB-1998; 98US-0074789P.

PR 19-FEB-1998; 98US-0075459P.

PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
 PR 19-FEB-1998; 98US-0075462P.
 PR 19-FEB-1998; 98US-0075463P.
 PR 19-FEB-1998; 98US-0075464P.
 PR 06-MAR-1998; 98US-0076912P.
 PR 09-MAR-1998; 98US-0077229P.
 PR 09-MAR-1998; 98US-0077230P.
 PR 09-MAR-1998; 98US-0077231P.
 PR 18-MAR-1998; 98US-0078368P.
 PR 07-APR-1998; 98US-0080844P.
 PR 27-APR-1998; 98US-0083067P.
 PR 29-APR-1998; 98US-0083386P.
 PR 29-APR-1998; 98US-0083387P.
 PR 29-APR-1998; 98US-0083388P.
 PR 29-APR-1998; 98US-0083389P.
 PR 29-APR-1998; 98US-0083390P.
 PR 13-MAY-1998; 98US-0085222P.
 PR 13-MAY-1998; 98US-0085223P.
 PR 13-MAY-1998; 98US-0085224P.
 PR 21-MAY-1998; 98US-0086183P.
 PR 21-MAY-1998; 98US-0086184P.
 PR 21-MAY-1998; 98US-0086185P.
 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089810P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
 PR 09-SEP-1998; 98US-0093667P.
 PR 09-SEP-1998; 98US-0093670P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
 PR 21-SEP-1998; 98US-0101132P.
 PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.

(CHEI/) CHEIKH N.

PA (FISH/) FISHER D K.

PA (LIUJ/) LIU J.

PI Cheikh N, Fisher DK, Liu J;

XX WPI; 2003-688722/65.

XX New maize or soybean enzymes and nucleic acid molecules associated with
 PT the sucrose pathway, useful for genome mapping, gene identification and

PT analysis, plant breeding, or preparation of constructs for plant gene expression.

BS Claim 2; Page; 117pp; English.

XX The invention relates to a substantially purified nucleic acid molecule (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme or its fragment, associated with the sucrose pathway selected from: CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase, CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent fructose-6-phosphate phosphotransferase, invertase, sucrose synthase, hexokinase, fructose kinase, UDP-glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine diphosphate (UDP)-glucose pyrophosphorylase. Also included are a CC substantially purified maize or soybean enzyme (or its fragment) and a CC transformed plant having a nucleic acid molecule. Also disclosed as new CC are purified antibodies capable of specifically binding to the maize or CC soybean enzyme, determining a level or pattern of a plant sucrose pathway CC enzyme in a plant cell or plant tissue, determining a mutation in a plant CC whose presence is predictive of a mutation affecting the level or pattern CC of a plant sucrose pathway enzyme, producing a plant containing an CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing CC expression of a plant sucrose pathway enzyme in a plant and determining CC an association between a polymorphism and a plant trait. The maize or CC soybean enzymes and nucleic acid molecules are useful for genome mapping, CC gene identification and analysis, plant breeding, or preparation of CC constructs for plant gene expression and transgenic plants. The nucleic CC acid molecules are also useful as markers or probes. The present sequence CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose CC pathway enzyme. Note: The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic format CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX Sequence 297 BP; 92 A; 51 C; 65 G; 89 T; 0 U; 0 Other;

Query Match 5.7%; Score 158; DB 8; Length 297;

Best Local Similarity 99.2%; Pred. No. 2.4e-52;

Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1122 TAAGAAATGATATCAGATTTCATGTCGTCATATCTGAGCAATTTCTGAGGATGC 1181

Db 2 TAAGAAATGATATCAGATTTCATGTCGTCATATCTGAGCAATTTCTGAGGATGC 61

QY 1182 TGCTGTGAATTCCTCTCAATTAACAAGCTACTCCAGACTTCATATTTGGAACATACAG 1241

Db 62 TGCTGTGAATTCCTCTCAATTAACAAGCTACTCCAGACTTCATATTTGGAACATACAG 121

QY 1242 TGATGAAATCTTGTGGCGTCATTTGCTATCTTACAAGATGGGAATACCCAGTGCACAT 1301

Db 122 TGATGAAATCTTGTGGCGTCATTTGCTATCTTACAAGATGGGAATACCCAGTGCACAT 181

QY 1302 TGCTCATGCTCTGAAAGACTAGTATCCAGATTCAGACATATTTGGGAATTTTGA 1361

Db 182 TGCTCATGCTCTGAAAGACTAGTATCCAGATTCAGACATATTTGGGAATTTTGA 241

QY 1362 TGAGAGTACCATTTCTCT 1381

Db 242 TGAGAGTACCATTTCTCT 261

RESULT 11

ADA58373

ID ADA58373 standard; cDNA; 150 BP.

XX ADA58373;

XX 20-NOV-2003 (first entry)

XX Maize sucrose synthase EST #17.

XX Plant; sb; EST; expressed sequence tag; transgenic; sucrose pathway;

KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;

KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase; phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase; pyrophosphate-dependent fructose-6-phosphate phosphotransferase; invertase; sucrose synthase; hexokinase; fructokinase; nucleoside diphosphate kinase-kinase; NDP; glucose-6-phosphate 1-dehydrogenase; phosphoglucose mutase; UDP; uridine diphosphate-glucose pyrophosphorylase; maize.

OS Zea mays.

XX US2003135870-A1.

PN 17-JUL-2003.

PD 26-JAN-1999; 99US-00237183.

XX 24-NOV-1997; 97US-0067000P.

PR 03-DEC-1997; 97US-0069472P.

PR 27-JAN-1998; 98US-0072888P.

PR 10-FEB-1998; 98US-0074201P.

PR 10-FEB-1998; 98US-0074280P.

PR 10-FEB-1998; 98US-0074281P.

PR 10-FEB-1998; 98US-0074282P.

PR 12-FEB-1998; 98US-0074565P.

PR 12-FEB-1998; 98US-0074566P.

PR 12-FEB-1998; 98US-0074567P.

PR 13-FEB-1998; 98US-0074789P.

PR 13-FEB-1998; 98US-0075459P.

PR 13-FEB-1998; 98US-0075460P.

PR 13-FEB-1998; 98US-0075461P.

PR 13-FEB-1998; 98US-0075462P.

PR 13-FEB-1998; 98US-0075463P.

PR 13-FEB-1998; 98US-0075464P.

PR 06-MAR-1998; 98US-0076912P.

PR 09-MAR-1998; 98US-0077229P.

PR 09-MAR-1998; 98US-0077230P.

PR 09-MAR-1998; 98US-0077231P.

PR 18-MAR-1998; 98US-0078368P.

PR 07-APR-1998; 98US-0080844P.

PR 27-APR-1998; 98US-0083067P.

PR 29-APR-1998; 98US-0083386P.

PR 29-APR-1998; 98US-0083387P.

PR 29-APR-1998; 98US-0083388P.

PR 29-APR-1998; 98US-0083389P.

PR 29-APR-1998; 98US-0083390P.

PR 13-MAY-1998; 98US-0085222P.

PR 13-MAY-1998; 98US-0085223P.

PR 13-MAY-1998; 98US-0085224P.

PR 21-MAY-1998; 98US-0086183P.

PR 21-MAY-1998; 98US-0086184P.

PR 21-MAY-1998; 98US-0086185P.

PR 21-MAY-1998; 98US-0086186P.

PR 21-MAY-1998; 98US-0086187P.

PR 21-MAY-1998; 98US-0086188P.

PR 01-JUN-1998; 98US-0087422P.

PR 16-JUN-1998; 98US-0089524P.

PR 18-JUN-1998; 98US-0089793P.

PR 18-JUN-1998; 98US-0089810P.

PR 18-JUN-1998; 98US-0089814P.

PR 22-JUN-1998; 98US-0090170P.

PR 26-JUN-1998; 98US-0090928P.

PR 29-JUN-1998; 98US-0091035P.

PR 30-JUN-1998; 98US-0091405P.

PR 08-JUL-1998; 98US-0092036P.

PR 09-SEP-1998; 98US-0099667P.

PR 09-SEP-1998; 98US-0099670P.

PR 09-SEP-1998; 98US-0099677P.

PR 16-SEP-1998; 98US-0100672P.

PR 16-SEP-1998; 98US-0100673P.

PR 16-SEP-1998; 98US-0100674P.

PR 21-SEP-1998; 98US-0101130P.

PR 21-SEP-1998; 98US-0101131P.

PR 21-SEP-1998; 98US-0101132P.

PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 25-SEP-1998; 98US-0101508P.
 PR 13-OCT-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-02199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.
 XX

PA (CHEI/) CHEIKH N.
 PA (FISH/) FISHER D K.
 PA (LIU/) LIU J.

PI Cheikh N, Fisher DK, Liu J;
 XX WPI; 2003-688722/65.

XX New maize or soybean enzymes and nucleic acid molecules associated with
 PT the sucrose pathway, useful for genome mapping, gene identification and
 PT analysis, plant breeding, or preparation of constructs for plant gene
 PT expression.

XX Claim 2; Page; 117pp; English.

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 CC (appearing as ADA57847 - ADA0660 that encodes a maize or soybean enzyme
 CC or its fragment, associated with the sucrose pathway selected from:
 CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
 CC transformed plant having a nucleic acid molecule. Also disclosed as new
 CC are purified antibodies capable of specifically binding to the maize or
 CC soybean enzyme, determining a level or pattern of a plant sucrose pathway
 CC enzyme in a plant cell or plant tissue, determining a mutation in a plant
 CC whose presence is predictive of a mutation affecting the level or pattern
 CC of a plant sucrose pathway enzyme, producing a plant containing an
 CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing
 CC expression of a plant sucrose pathway enzyme in a plant and determining
 CC an association between a polymorphism and a plant trait. The maize or
 CC soybean enzymes and nucleic acid molecules are useful for genome mapping,
 CC gene identification and analysis, plant breeding, or preparation of
 CC constructs for plant gene expression and transgenic plants. The nucleic
 CC acid molecules are also useful as markers or probes. The present sequence
 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX Sequence 150 BP; 39 A; 39 C; 29 G; 43 T; 0 U; 0 Other;

Query Match 5.4%; Score 150; DB 8; Length 150;
 Best Local Similarity 100.0%; Pred. No. 3.8e-49;
 Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 ACCGAGTTGCCATGGATCGATCTTCGATCCAAAGTTCATATAGTCTCTCTCGAG 1576
 |||||||
 Db 1 ACCGAGTTGTCATGGATCGATCTTCGATCCAAAGTTCATATAGTCTCTCTCGAG 60
 |||||||

QY 1577 CTGACATGTCATATACCTTTCCATACCGAGAGGCCAAGCGACTCACCTCTCTTCATG 1636

Db 61 CTGACATGTCATATACCTTTCCATACCGAGAGGCCAAGCGACTCACCTCTCTTCATG 120
 |||||||
 QY 1637 GTTCAATCGAAAATTGATTTATGACCCGG 1666
 |||||||
 Db 121 GTTCAATCGAAAATTGATTTATGACCCGG 150
 |||||||

RESULT 12

ADA58864
 ID ADA58864 standard; cDNA; 411 BP.

XX ADA58864;

XX 20-NOV-2003 (first entry)

XX Maize sucrose synthase EST #508.

XX Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
 KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucose mutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.

XX Zea mays.

XX US2003135870-A1.

XX 17-JUL-2003.

XX 26-JAN-1999; 99US-00237183.

XX 24-NOV-1997; 97US-0067000P.

XX 09-DEC-1997; 97US-0069472P.

XX 27-JAN-1998; 98US-0072888P.

XX 10-FEB-1998; 98US-0074201P.

XX 10-FEB-1998; 98US-0074281P.

XX 12-FEB-1998; 98US-0074282P.

XX 12-FEB-1998; 98US-0074565P.

XX 12-FEB-1998; 98US-0074566P.

XX 12-FEB-1998; 98US-0074567P.

XX 19-FEB-1998; 98US-0074569P.

XX 19-FEB-1998; 98US-0075459P.

XX 19-FEB-1998; 98US-0075460P.

XX 19-FEB-1998; 98US-0075461P.

XX 19-FEB-1998; 98US-0075462P.

XX 19-FEB-1998; 98US-0075463P.

XX 19-FEB-1998; 98US-0075464P.

XX 06-MAR-1998; 98US-0076912P.

XX 09-MAR-1998; 98US-0077229P.

XX 09-MAR-1998; 98US-0077231P.

XX 18-MAR-1998; 98US-0078368P.

XX 07-APR-1998; 98US-0080844P.

XX 27-APR-1998; 98US-0083067P.

XX 29-APR-1998; 98US-0083386P.

XX 29-APR-1998; 98US-0083387P.

XX 29-APR-1998; 98US-0083388P.

XX 29-APR-1998; 98US-0083389P.

XX 29-APR-1998; 98US-0083390P.

XX 13-MAY-1998; 98US-0085222P.

XX 13-MAY-1998; 98US-0085223P.

XX 13-MAY-1998; 98US-0085224P.

XX 21-MAY-1998; 98US-0086183P.

XX 21-MAY-1998; 98US-0086184P.

XX 21-MAY-1998; 98US-0086185P.

XX 21-MAY-1998; 98US-0086186P.

XX 21-MAY-1998; 98US-0086187P.

PR 21-MAY-1998; 98US-0086189P.
 PR 01-JUN-1998; 98US-0087422P.
 PR 16-JUN-1998; 98US-0089524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089813P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 22-JUN-1998; 98US-0090170P.
 PR 26-JUN-1998; 98US-0090928P.
 PR 29-JUN-1998; 98US-0091035P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 08-JUL-1998; 98US-0092036P.
 PR 09-SEP-1998; 98US-0099667P.
 PR 09-SEP-1998; 98US-0099670P.
 PR 09-SEP-1998; 98US-0099679P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
 PR 21-SEP-1998; 98US-0101132P.
 PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104123P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-0019912P.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0112224P.
 PR 12-JAN-1999; 98US-00229413.
 XX
 PA (CHEI/) CHEIKH N.
 PA (FISH/) FISHER D K.
 PA (LIU/) LIU J.
 XX
 PI Cheikh N, Fisher DK, Liu J;
 XX WPI; 2003-688722/65.
 XX
 PT New maize or soybean enzymes and nucleic acid molecules associated with
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 PT analysis, plant breeding, or preparation of constructs for plant gene
 PT expression.
 XX
 PS Claim 2; Page; 117pp; English.
 XX
 CC The invention relates to a substantially purified nucleic acid molecule
 CC (appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme
 CC or its fragment, associated with the sucrose pathway selected from:
 CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose
 CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,
 CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent
 CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,
 CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,
 CC glucose-6-phosphate 1-dehydrogenase, phosphoglucose mutase and uridine
 CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a
 CC substantially purified maize or soybean enzyme (or its fragment) and a
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 CC are purified antibodies capable of specifically binding to the maize or
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 CC an association between a polymorphism and a plant trait. The maize or

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 CC is a maize EST (expressed sequence tag) from a gene encoding a sucrose
 CC pathway enzyme. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
 XX
 SQ Sequence 411 BP; 99 A; 109 C; 113 G; 88 T; 0 U; 2 Other;
 Query Match 5.2%; Score 143; DB 8; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1759 GGGCTGGTCAAGCTTTTCTAAGTCGCTAAGTCAGGAGCTGTAAACCTTTCGTC 1818
 DB 88 GGGCTGGTCAAGCTTTTCTAAGTCGCTAAGTCAGGAGCTGTAAACCTTTCGTC 147
 QY 1819 GTTCCGGGTACAAATGATCTCAACAGTCCAGGACAGGAGAGATCGCGGAGATAGAG 1878
 DB 148 GTTCCGGGTACAAATGATCTCAACAGTCCAGGACAGGAGAGATCGCGGAGATAGAG 207
 QY 1879 AAGATGCATGAACCTCATCAAGAC 1901
 DB 208 AAGATGCATGAACCTCATCAAGAC 230
 RESULT 13
 ADA58374
 ID ADA58374 standard; cDNA; 255 BP.
 XX
 AC ADA58374;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Maize sucrose synthase EST #18.
 XX
 KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;
 KW triose phosphate isomerase; fructose 1; 6-bisphosphate aldolase;
 KW fructose 1; 6-bisphosphate; fructose 6-phosphate 2-kinase;
 KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;
 KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;
 KW invertase; sucrose synthase; hexokinase; fructokinase;
 KW nucleoside diphosphate kinase-kinase; NDP;
 KW glucose-6-phosphate 1-dehydrogenase; phosphoglucose mutase; UDP;
 KW uridine diphosphate-glucose pyrophosphorylase; maize.
 XX
 OS Zea mays.
 XX
 PN US2003135870-A1.
 XX
 PD 17-JUL-2003.
 XX
 XX 26-JAN-1999; 98US-00237183.
 XX
 XX 24-NOV-1997; 97US-0067000P.
 PR 09-DEC-1997; 97US-0069472P.
 PR 27-JAN-1998; 98US-0072888P.
 PR 10-FEB-1998; 98US-0074201P.
 PR 10-FEB-1998; 98US-0074280P.
 PR 10-FEB-1998; 98US-0074281P.
 PR 10-FEB-1998; 98US-0074282P.
 PR 12-FEB-1998; 98US-0074565P.
 PR 12-FEB-1998; 98US-0074566P.
 PR 12-FEB-1998; 98US-0074567P.
 PR 19-FEB-1998; 98US-0074789P.
 PR 19-FEB-1998; 98US-0075459P.
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06-MAR-1998; PR 98US-0076912P.
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18-MAR-1998; PR 98US-0078316P.
18-MAR-1998; PR 98US-0078318P.
27-APR-1998; PR 98US-0080844P.
27-APR-1998; PR 98US-0081067P.
29-APR-1998; PR 98US-0083386P.
29-APR-1998; PR 98US-0083387P.
29-APR-1998; PR 98US-0083388P.
29-APR-1998; PR 98US-0083389P.
29-APR-1998; PR 98US-0083390P.
13-MAY-1998; PR 98US-0085222P.
13-MAY-1998; PR 98US-0085223P.
13-MAY-1998; PR 98US-0085224P.
21-MAY-1998; PR 98US-0086183P.
21-MAY-1998; PR 98US-0086184P.
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21-MAY-1998; PR 98US-0086187P.
21-MAY-1998; PR 98US-0086188P.
01-JUN-1998; PR 98US-0087422P.
16-JUN-1998; PR 98US-0089524P.
18-JUN-1998; PR 98US-0089793P.
18-JUN-1998; PR 98US-0089810P.
18-JUN-1998; PR 98US-0089811P.
22-JUN-1998; PR 98US-0090170P.
26-JUN-1998; PR 98US-0090928P.
29-JUN-1998; PR 98US-0091035P.
30-JUN-1998; PR 98US-0091405P.
08-JUL-1998; PR 98US-0092035P.
09-SEP-1998; PR 98US-0099667P.
09-SEP-1998; PR 98US-0099670P.
09-SEP-1998; PR 98US-0099697P.
16-SEP-1998; PR 98US-0100672P.
16-SEP-1998; PR 98US-0100673P.
16-SEP-1998; PR 98US-0100674P.
21-SEP-1998; PR 98US-0101130P.
21-SEP-1998; PR 98US-0101131P.
21-SEP-1998; PR 98US-0101132P.
22-SEP-1998; PR 98US-0101343P.
22-SEP-1998; PR 98US-0101344P.
22-SEP-1998; PR 98US-0101347P.
22-SEP-1998; PR 98US-0101508P.
25-SEP-1998; PR 98US-0101707P.
13-OCT-1998; PR 98US-0104123P.
13-OCT-1998; PR 98US-0104124P.
13-OCT-1998; PR 98US-0104126P.
13-OCT-1998; PR 98US-0104127P.
13-OCT-1998; PR 98US-0104128P.
18-NOV-1998; PR 98US-0108996P.
19-NOV-1998; PR 98US-0109018P.
24-NOV-1998; PR 98US-0019912P.
08-DEC-1998; PR 98US-0021023T.
11-DEC-1998; PR 98US-0111981P.
22-DEC-1998; PR 98US-0113224P.
12-JAN-1999; PR 98US-00229413.

(CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIU/) LIU C.

Cheikh N., Fisher DK., Liu J;
WPI; 2003-688722/65.

New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene expression.

Claim 2; Page: 117pp; English.

ABX83402
ID ABX83402 standard; cDNA; 265 BP.

XX AC ABX83402;

XX DT 24-APR-2003 (first entry)

XX DE Corn ear-derived polynucleotide (cpd) #1862.

XX KW Corn ear-derived polynucleotide; cpd; cDNA library; SATMON022; SATMON023;
XX structural gene; functional gene; regulatory gene;
XX corn ear-specific profile; gene transcription; gene expression;
XX hybrid plant; desirable trait expression; plant breeding program;
XX inheritance; desired characteristic; growth; development;
XX disease resistance; environmental adaptability; quality; yield;
XX multigene trait; plant; gene; ss.

XX OS Zea mays.

XX PN US6476212-B1.

XX PD 05-NOV-2002.

XX PF 14-MAY-1999; 99US-00313294.

XX PR 26-MAY-1998; 98US-0086722P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Lalgudi RV, Ito LY, Sherman BK;

XX DR WPI; 2003-208840/20.

XX PT Novel purified corn-ear derived polynucleotide useful as hybridization
PT probe for detecting polynucleotide in sample, and for identifying,
PT evaluating, and altering desired characteristics associated with growth,
PT development.

XX PS Example; SEQ ID NO 1862; 390pp; English.

XX CC The present invention relates to the isolation of corn ear-derived
CC polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022
CC and SATMON023. Some of the cdps uniquely identify structural, functional,
CC and regulatory genes of corn ear. The polynucleotides sequences are
CC useful for detecting cdps in a sample, for producing a corn ear-specific
CC profile of gene transcription, for detecting altered gene expression in
CC inbred or hybrid plants, and for screening several molecules for specific
CC binding to the polynucleotide. The cdps are useful to identify, isolate,
CC or extend identical or related corn-ear nucleic acid sequences from DNA
CC libraries, and in nucleic acid amplification or hybridisation techniques
CC to follow the expression of desirable traits through plant breeding
CC programs. Preferably, the cdps are used to identify, evaluate, alter, or
CC follow the inheritance of desired characteristics associated with growth
CC and development, disease resistance, environmental adaptability, quality,
CC and yield of corn. The cdps are also useful as molecular markers for
CC studying inheritance and multigene traits in a plant breeding program.
CC The cdps are useful for producing purified corn-ear polypeptides by
CC recombinant techniques. They are also useful in diagnostic assays to
CC detect or confirm conditions or diseases associated with abnormal levels
CC of cdp expression. ABX81541-ABX89140 represent corn ear-derived
CC polynucleotides (cdps) of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdIDentry.html

XX SQ Sequence 265 BP; 65 A; 63 C; 71 G; 66 T; 0 U; 0 Other;

Query Match 4.4%; Score 122; DB 7; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.8e-38;
Matches 122; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 110 ATGATAGATAAAGCTTTGGGAGGCTTCAGTCTGCTGACCAAAAGCTGAGGAGCACT 169
QY 644 TGTCAAAGCTCCCTGCTGACACACATACCTCACAATTTGCTTATAAATTCAGAGTGGS 703
Db 170 TGTCAAAGCTCCCTGCTGACACACATACCTCACAATTTGCTTATAAATTCAGAGTGGS 229
QY 704 GC 705
Db 230 GC 231

Search completed: May 26, 2004, 02:50:35
Job time : 697.021 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n.mcd1

Run on: May 26, 2004, 12:48:39 ; Search time 130.937 Seconds
(without alignments)
4447.890 Million cell updates/sec

Title: US-10-080-114A-12

Perfect score: 4247

Sequence: 1 MSAPKLNRRASIRDRVEDTL.....YILKFRRLAKTVPALDQPO 809

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1363418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q/cgn2_1/USFTO.spool/US10080114/runat.24052004.112230.20414/app.query.fasta_1.1934

-DB-issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPEL=0

-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.cdi

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-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2_6/ptodata/2/ira/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ira/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ira/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
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2	2892.5	68.1	3103	4	US-09-598-431C-57
3	2452	57.7	6386	2	US-08-483-376-
4	1833	43.2	2700	4	US-08-684-025-
5	444	10.5	3509	1	US-08-175-471-6
6	444	10.5	3509	2	US-08-718-777-6
7	444	10.5	3509	3	US-09-078-862-2
8	444	10.5	3509	3	US-09-251-341-6
9	444	10.5	3509	4	US-09-866-153-12
10	444	10.5	3509	4	US-09-693-467A-12
11	441.5	10.4	3625	1	US-08-356-354-3
12	441.5	10.4	3625	2	US-08-778-656-3

13	441.5	10.4	3635	2	US-08-553-436A-5
14	436	10.3	3509	2	US-08-429-054A-12
15	420	9.9	3524	4	US-09-697-367-15
16	413.5	9.7	265	4	US-09-313-294A-1862
17	408	9.6	3539	3	US-08-853-948B-1
18	396	9.3	3740	1	US-08-356-354-1
19	396	9.3	3740	2	US-08-778-656-1
20	365	8.6	271	4	US-09-313-294A-1826
21	355	8.4	532	4	US-09-598-401C-56
22	328	7.7	272	4	US-09-313-294A-1221
23	307	7.2	2930	1	US-08-356-354-5
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27	186	4.4	210	3	US-09-125-384-1
28	180.5	4.3	282	4	US-09-313-294A-427
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31	173.5	4.1	661	4	US-09-697-367-9
32	170	4.0	4403765	3	US-09-103-840A-2
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34	165	3.9	1524	4	US-09-134-001C-1141
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44	136.5	3.2	2067	4	US-09-388-743-21
45	134.5	3.2	1167	4	US-09-489-039A-999

ALIGNMENTS

RESULT 1

US-08-553-436A-7

; Sequence 7, Application US/08553436A

; Patent No. 5866790

; GENERAL INFORMATION:

; APPLICANT: HESSE, Holger

; APPLICANT: MULLER-ROBER, Bernd

; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

; TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE

; TITLE OF INVENTION: CONCENTRATION

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen

; STREET: 1180 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10036-8403

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/553,436A

; FILING DATE: 17-NOV-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP94/01671

; FILING DATE: 20-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 4317596.1

; FILING DATE: 24-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Meilman, Edward

; REGISTRATION NUMBER: 24,735

1689 AATGACAGGAGGAATTCGCCAAATCGACGAAGATGACACAGGCTTATACAGGATATAAT 1748
Qy
637 LeuPheGlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeu 656
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2226 CTGGCCAACTCTGTCGCTGGCAACAGATGAA 2258

RESULT 2

US-09-598-401C-57
; Sequence 57, Application: US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Ragleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.10362
; CURRENT APPLICATION NUMBER: US/09/598,401C
; PRIORITY FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 03/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 3103
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-57

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Score: 2892.50 Matches: 540
Percent Similarity: 81.78% Conservative: 120
Best Local Similarity: 66.91% Mismatches: 144
Query Match: 68.11% Indels: 3
DB: 4 Gaps: 2

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361 TyrIleLeuArgValProPheArgAsnGluAsnGlyIleLeuLysTyrTrpIleSerArg 380
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481 TyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGluSerHisThrAlaPhe 500
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501 ThrLeuProGlyLeuTyrArgValValHisGlyIleAspValPheAspProLysPheAsn 520
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2247 CTGCGCACTTGTGCTGTGTGAGGT-----GACAGGAGGAGGATTCGAGGACTTG 2300
620 GluGluIleAlaGluLeuGluLysMetHisGluLeuIleLysThrHisAsnLeuPheGly 639
2301 GAGAGCAGCTCAGATGAAGAAATGTACGACCTCATCGAAAGTACAAAGCTGAATGCG 2360
640 GlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArgTyr 659
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660 IleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeuThr 679
2421 ATCTGTGACAGAAAGGAGTCTCGTTACACCGCTATCTATGAGCTTTCGGTTGACC 2480
680 ValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyProAla 699
2481 GTGGTTGAGGCCATGACTTGTGATTCGCAACCTTTCGCCATTCGATGTCGACACAGCT 2540
700 GluIleIleGluHisGlyValSerGlyPheHisIleAspProTyrHisProGluGlnAla 719
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2601 GCCAGCTTCTTGTAGACTTCTTCAAGAGTCAAGATGACCACTCCCACTGGACGAG 2660
740 IleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTrpLysIleTyrSerGlu 759
2661 ATCTCAAGGTCCTCATGACAGAAATGAAGAGAGATATACATCGAAATATATTTCTGAG 2720
760 ArgLeuMetThrLeuAlaGlyValTyrGlyPheTrpLysTyrValSerLysLeuGluArg 779
2721 AGGCTGTGAACCTGACTGCCGTGTATGGCTTCTGGAAGCATGTGACTTAACCTTGCATCG 2780
780 LeuGluThrArgArgTyrLeuGluMetPheTyrIleLeuLysPheArgGluLeuAlaLys 799
2781 CGGAGAGTCCCGGTACCTTGAATGTTCTATGCCCTCAAGTATCGCCCACTGGACAG 2840
800 ThrValProLeuAlaIleAsp 806
2841 TCTGTCTCTCCGCTGTGCGAG 2861

RESULT 3
US-08-483-376-1
; Sequence 1, Application US/08483376
; Patent No. 5955330
; GENERAL INFORMATION:
; APPLICANT: Vasil, Vimla
; APPLICANT: Clancy, Maureen A.
; APPLICANT: Perl, Robert J.
; APPLICANT: Vasil, Indra K.
; APPLICANT: Hannah, L. C.
; TITLE OF INVENTION: No. 5955330el Means for Enhancing Gene
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Wimmer and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,376
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/418,540
; FILING DATE: 07-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,115
; FILING DATE: 04-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/830,956
; FILING DATE: 05-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/353,854
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 10-94B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6386 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double


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QY 296 LeuProAspThrGlyGly----- 301
Db 3018 TACCCTGACACTGGCGTCAGGTACAGAGCTTAGTGATTACTATTTCCTTTAGGCTTGG 3077
QY 301 ----- 301
Db 3078 TTTGGGTATAGAGGATTCGAAGTGAATTGAGGTGTATTAAAGAGGATTGAAGAAAAATT 3137
QY 301 ----- 301
Db 3138 AGTTTATATTACATTCAATACACCAATACCACTCAATCCACTCAATTGAGATTAC 3197
QY 302 -----Gln11 303
Db 3198 CCMAACAAGCCCTTAGCTACTTTCCACTTCCAGGTTTCTCATTTGGCATCGTTGCGGT 3257
QY 303 eValTyrlleLeuAspGlnValIargAlaLeuGluAsnGluMetValLeuArgLeuLysLy 323
Db 3258 TGTGTACATTCTGGATCAGGTCGCTTTGGAGAAATGAGATGCTTCTGAGGATTAAAGCA 3317
QY 323 sGlnGlyLeuAspValSerProLysIleLeuIle----- 334
Db 3318 GCAGGCCCTTGATACCTCCGAAGATCCTCAT-TGTAATGTTTGAGCCCAAGCTTCACT 3376
QY 334 ----- 334
Db 3377 TCTGAATCCTTTTTTCACTGTGCTTGATTTTACTCAGTAAATGTCCTACATGATCTTA 3436
QY 335 -----ValThrArgLeuIleProAspAlaLysGlyThrSerCysAsnGlnArgLe 351
Db 3437 TTTGTTGAGGTTTACAGGCTGTGCTGATGCTGCTGGAGTACATCGCGGTGAGCGCT 3496
QY 351 uGluArgIleSerGlyThrGlnHisThrTyrlleLeuArgValProPheArgAsnGluAs 371
Db 3497 GAGAGGTCATTGTTACTGAGCACACACATCATTCGGTTCCTTTCGAAATGAGAA 3556
QY 371 nGlyIleLeuLysLysTrpIleSerArgPheAspValTrpProTyrlleLeuGluThrPheAl 391
Db 3557 TGGCATCCTCCGAAGTGGATCTCTGTTTGATGTCGGCCATACCTGGCCATACCTGGAGCATACAC 3616
QY 391 aglu----- 392
Db 3617 TGAAGTATACCGATTATCTGACTGGATGCTCTACACAGCATAGCATGTTTGAGTAATATAC 3676
QY 393 -----AspAlaalaGlyGluIleAlaalaGluLeuGlnG 404
Db 3677 TGAAGCCATGCATTCTGTCTGCAGGATGTTTCCAGTGAATTAATGAAGAAATGACGGC 3736
QY 404 yThrProAspPheIleIleGlyAsnTyrlSerAspGlyAsnLeuValAlaSerLeuLeuSe 424
Db 3737 CTAAGCTGACCTTATCATTTGGCAACTACAGCGATGGCAACCTAGTCGCCACTCTGCTGCG 3796
QY 424 rTyrlsMetGlyIleThr----- 430
Db 3797 GCACAAGTTGGAGTCACTCAGTCTGTCTGTTGGTTTTTACATGATATTTGAGTATCT 3856
QY 431 -----GlnCysAs 433
Db 3857 TTAATAATATTAGTTATTATTTCATTGCTTAAATGTTTTGTATACATCTTGAGTGTAC 3916
QY 433 nIleAlaHisAlaLeuGluLysThrLysTyrlProAspSerAspIlePheTrpLysAsnPh 453
Db 3917 CATCGCTCATGCTTGAGAGAAACCAATACCCCAACTCGACATATATCTTGACAAATT 3976
QY 453 eAspGluLysTyrlHisPheSerCysGlnPheThrAaAspIleAlaMetAsnAl 473
Db 3977 CGACACCGAGTACCACTTCTTTGCCAGTTTCACAGCTGACCTTATTGCCATGAACACAC 4036
QY 473 aAspPheIleIleThrSerThrTyrlGlnGluIleAlaGly----- 486
Db 4037 CGATTTTCATCACCAGCACATTCGAAGAAATCGCGGAAGGTAGAAATTTGTATATTAG 4096
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QY 487 -----S 487
Db 4097 TAGCTGTGCTTTAGTAGTAAATAAAACTAGTATGTATGTATCTTTCTGTGTGTTCTGCA 4156
QY 487 eTyrlsAsnThrValGlyGlnTyrlGluSerHisThrAlaPheThrLeuProGlyLeuTyra 507
Db 4157 GCAAGACACCGTGGGCGCAGTACAGTCCACATCGCGTTCACTTCTTCTGGGCTCTACC 4216
QY 507 zGValValHisGlyIleAspValPheAspProLysPheAsnIleValSerProGlyAlaA 527
Db 4217 GTGTCTCCATGATCGATCGATGTTTTCATCCCAAGTTCAACATTTCTCCCTCGAGCAG 4276
QY 527 sPmetSerIleTyrlPheProHisThrGluLysAlaLysArgLeuThrSerLeuHisGlyS 547
Db 4277 ACATGAGTGTTHACTACCGGTATACGGAACCCGACAGAGACTCACTGCCTTCCATCTCG 4336
QY 547 eTrIleGluAsnLeuIleTyrlAspProGluGlnAsnAspGluHis----- 561
Db 4337 AAATCGAGGAGCTCATCTACAGCGAGTCCGAGAACTCCGAGACCAAGTGAGTATACTGAA 4396
QY 561 ----- 561
Db 4397 AACTGTTGCATGCTTACTGCGAGCAATCAGCTTGTAAATACTCCAAACCCATCGCAT 4456
QY 562 -----IleGlyHisLeuAsp----- 566
Db 4457 GATCTATCCATCTTTCTATCTGTCACTTGAG-CTGAACACCTGCTGTTTACTTGCATCCA 4515
QY 567 -----AspArgSerLysProIleLeuPheSerMetAlaArgLeuAspArgV 582
Db 4516 GSTTGTGCTGAAGGACAAAGAACCGCATCATCTTCTCGATGGCGCTCTCGACCGCG 4575
QY 582 allysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeuArgGluLeuV 602
Db 4576 TGAAGAACATGACAGCGCTGCTGAGATGTCGGCAGAACCGCGCTCGAGGAGCTGG 4635
QY 602 aLasnLeuValValAlaGlyTyrlAsnAspValAsnLysSerLysAspArgGluGluI 622
Db 4636 CGAACTCTGTGATCGTTGCGGT---GACCACGCGAAGGAGTCCNAGACAGGAGGAGGC 4692
QY 622 leAlaGluIleGluLysMetHisGluIleLysThrHisAsnLeuPheGlyGlnPheA 642
Db 4693 AGCGGAGTTCAGAAGATGTACAGCTCTCATCGCAGTACAAAGTTTGAAGCGCCATATCC 4752
QY 642 rGTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrlArgTyrlleAlaA 662
Db 4753 GGTGGATCTCGGCGCAGATGAACCGGTCCGCAACGCGGAGCTGTACCGCTACATTTGG 4812
QY 662 sPThrHisGlyAlaPheValGln----- 669
Db 4813 ATACGAAGGCGCGATTTCGTGAGGTATATGCACACACACACACTTGGATCTAATAT 4872
QY 669 ----- 669
Db 4873 CTAACTCCCAAGTTCCCAACAGCTGCAATCTACTTTTCAGACACACACAGTCACGTGAAT 4932
QY 670 -----ProAlaLeuTyrlGluAlaPheGlyL 678
Db 4933 CATTTCACTCTTTGTTTTTTTTTTTGTGGTAGCTTGGTTCTACGAAGCGTTCCGCC 4992
QY 678 eUthrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyP 698
Db 4993 TGACTGTGATCGAGTCCATGACGTGCGGTCTGCCAACGATCGCGACTGTCATCGCGGCC 5052
QY 698 roAlaGluIleIleGluHisGlyValSerGlyPheHisIleAspProTyrlHisProGluG 718
Db 5053 CTGCTGAGATCATCTGCGAGCGGGTATCTGGCTGCACATTTGACCTTACACAGCGACA 5112
QY 718 lnaAlaValAsnLeuMetAlaAspPheAspArgCysLysGlnAspProAspHisTrpV 738
Db 5113 AGGCCCGGATATCTTGGTCACTTCTTTTGACAAATGCAAGGCGAGATCCGAGCTACTGG 5172
QY 738 aLasnIleSerGlyAlaGlyLeuGlnArgIleTyrlGluLys----- 751
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[illegible]

RESULT 4

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US-08-684-005-1
; Sequence 1, Application US/38694005
; Patent No. 6682918
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Buikema, William J.
; APPLICANT: Bauer, Christopher C.
; TITLE OF INVENTION: BACTERIAL SUCROSE SYNTHASE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,005
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARSB:508
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7377
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-684-005-1

Alignment Scores:
Pred. No.: 1,6e-201 Length: 2700
Score: 1893.00 Matches: 359
Percent Similarity: 66.33% Conservative: 163
Best Local Similarity: 45.62% Mismatches: 251
Query Match: 43.16% Indels: 14
DB: 4 Gaps: 7

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Query Match: 10.45% Indels: 164
DB: 1 Gaps: 24

US-10-080-114a-12 (1-809) x US-08-175-471-6 (1-3509)

241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGlnAla 260
|||||
532 GGAGACACCATCGCGAGCTT-----GCG 555

261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276
|||||
556 CCGGTTGAGACGACCAAGAGAGTTCACAGAGAACCTCTCTGACCTTACCGCTCTGGTCT 615

277 -----PheAsnValValValValValSerProHisGlyTyrPhe--- 288
|||||
616 GACGACAAATAGGAGAGAGAGCTTACATCTGTCTCATCGCGTCATCGTCTTGGTCT 675

289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
|||||
676 GGAGAAACATGGAACTAGCTGATCTCATACAGTGGCCAGGTGAATATGTGGTC 735

308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysLysGlnGlyLeuAsp 327
:::
736 GAACCTTCAAGAGCG-----ATGTCA 756

328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
|||||
757 ATGATGCTGGAGTGTACAGGTGACCTTCTACTCTGTCAGTGTCAATCTCTCTGACGTG 816

342 -----AlaLysGlyThrSerCysAsnGlnArg 350
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817 GACTGGAGCTACGCTGAGCCCAACCGAGATGTTATCGCGCGCTTCCAATGATGGAGGGG 876

351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
:::
877 ATGGGTGAGAGTGGCGA-----GCCTACATTTGTGGCATAACCGTGT----- 918

371 AsnGlyIleLeuLysTyrIleSerArgPheAspValTyrProTyrLeuGluThrPhe 390
:::
919 ---GGCGCGGGGATATATACCTCAAGAGGAGCGTTGTGGCTTACCTCCAGAGTTT 975

391 AlaGluAspAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
:::
976 GTGATGAGCGCTTGGCATATCTGAACATGTCACAGCTCTGGGAGAGCAGTTTGA 1035

405 Thr-----ProAspPheIleIleGlyAsnTyrSerAspGlyAsnLeuVal 419
|||||
1036 AATGGGAGGCCAGTACTGCTTACGTGATATACGGCACATATGCGGATGCTGGAGATGT 1095

420 AlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu 439
:::
1096 CTGTCTCTCTTCTGCTGGCTGAATGTGCCATGTGCTCACTGGCCACTCACTTGGG 1155

440 LysThrLys-----TyrProAspSerAspIlePheTyrLysAsnPheAspGlu 455
:::
1156 AGGAACAAGCTGGACAACTGCTGAAGCAAGGGCGCATGTCACAGGAGAGATCGATTCG 1215

456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPhe 475
:::
1216 ACATACAAAGATCATGAGGCGGTATCAGGGGTGAGGCTGGACCTGGATGCTCAGAGCTT 1275

476 IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu 495
:::
1276 GTATACAGGACCAAGGAGGAGATGAT-----GAGCATGG--- 1314

496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal--- 514
:::
1315 -----GGATTGTAC-----GATGATTTGATGTCAAG 1341

515 -----PheAsp 516
:::
1342 CTTGAGAAAGTGTGAGGCGACCGGCGGGGTAGTCCCATGTTGCTTACATG 1401

517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
|||||
1402 CCTAGGATGGTGGTGAATTCCTCGGGAATGATTTTCAGCAATGTTGTAGTTCAI----- 1455

537 LysAlaLysArgLeuThrSerLeuHisGlySerIleGlyAsnLeuIleTyrAspProGlu 556
|||||
1456 -----GAAGACATTGATGGGATGGTAC 1479

557 GlnAsnAspGluHisIleGly----- 563
|||||
1480 GTCAAGATGATGATGTTGGTGGAGGGTGCCTCACCAGTCAATGCCCCCAATTGG 1539

564 -----HisLeuAspAspArgSerLysProIleLeuPheSerMetAlaArg 578
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1540 GCGAAGTGAATGGTCTCTGACCAACCTCAAGCCGATGATCTCTGGCGTTATCAAGA 1599

579 LeuAspArgValLysAsnIleThrGlyLeuValGlnAlaPheAlaLysCysAlaLysLeu 598
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1600 CCAGACCGAAGAGAACATCACTACCTCTCGTCAAGCGTTTGGAGAGTGTCTCCACTC 1659

599 ArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSerLysAsp 618
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1660 AGGAACTTGCAAACCTTACTCTGATCATCGGTAACAGAGATGACATCGACGACATGT 1719

619 ArgGluGlnIleAlaGluIleGluLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
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1720 GCTGGCATGGAGTCTCTCACCACAGTCTGAAGCTGATTCAGACAGTATGATCTGTAC 1779

639 GlyGlnPheArgTyrIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
:::
1780 GGAAGCGTGGCGTTC---CCTAAGCATCACAATCAGGTGACGTCCTCCGAGATCTATCGC 1836

659 TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
|||||
1837 CTCGCGGCAAAATGAAGGGGTCTTCATCAACCTGCTCTGCTGAGCGCTTGGTCTC 1896

679 ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
|||||
1897 ACCCTGATCGAGGCTGGCGCACACGACTCCGATGTCGCTACCAAGATGGTGGTCCG 1956

699 AlaGluIleIleGluHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
:::
1957 GTCGACATTACAAATGCACTAAACACGAGCTGCTCGTTGACCCACACGACGAG--- 2010

719 AlaValAsnLeuMetAlaAspPheAspArgCysLysGlnAspProAspHisTyrVal 738
|||||
2011 -----AACGCAATGCTGTGATGCACTGCTGAGGCTTGTGGCAGACAGAACCTGTGGCAG 2064

739 AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTyrLysIleTyrSer 758
|||||
2065 GAATGCGGAGAAACGGCTGCGCAATCCAC---CTCTACTCATGCGCGAGACCTGC 2121

759 GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTyrLysTyrValSerLysLeu 777
:::
2122 CGCACTTACCTCACCAGGTGCGCGGTGC----- 2151

778 GluArgLeuGluThrArgArgTyrIleGlu 787
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2152 ---CGTTAAGAAACCGAGGTGGCTGAAG 2178

RESULT 6

US-08-718-777-6
; Sequence 6, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
; APPLICANT: Van Assche, C.
; APPLICANT: Lando, D.
; APPLICANT: Bruneau, J. M.
; APPLICANT: Woelker, T.
; APPLICANT: Gervais, M.
; TITLE OF INVENTION: MODIFICATION OF SUCROSE
; TITLE OF INVENTION: PHOSPHATE
; TITLE OF INVENTION: SYNTHASE IN PLANTS

; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Barbara Rae-Venter
 ; STREET: 260 Sheridan Avenue, Suite 440
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: JS/08/718,777
 ; FILING DATE: NOT YET ASSIGNED
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JS 08/175,471
 ; FILING DATE: 27-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barbara Rae-Venter
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.072.02US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)328-4400
 ; TELEFAX: (415)328-4477
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3509 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 112..3315
 ; US-08-718-777-6

Alignment Scores:
 Pred. No.: 1,84e-40 Length: 3509
 Score: 444.00 Matches: 159
 Percent Similarity: 42.48% Conservative: 96
 Best Local Similarity: 25.24% Mismatches: 211
 Query Match: 10.45% Indels: 164
 DB: 2 Gaps: 24

US-10-080-114A-12 (1-809) x US-08-718-777-6 (1-3509)

QY	241	GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuAspIleIleGlnAla	260
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DB	556	CCGGTTGACAGCACCAAGAAAGTTCCAGAGAACTTCTCTGACCTTACCGCTCGGTCT	615
QY	277	-----PheAsnValValValValSerProHisGlyTyrPhe---	288
DB	616	GACGACAATAAGGAGAAGCTTTACATTGCTCATCGCGTGCATGCTTTGTTGCT	675
QY	289	GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu	307
DB	676	GGAGAAACATGGAACCTAGTCTGTGATTCTGATACAGGTGGCCAGGTGAATATGTGTC	735
QY	308	AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysGlnGlyLeuAsp	327
DB	736	GAACTTGCAAGAGCG-----ATGTCA	756
QY	328	ValSerPro-----LysIleLeuIleValThrArgLeuLeu-----ProAsp---	341
DB	757	ATGATCCCTGGAGTGATACAGGGTGGACCTCTTCACTCGTCAAGTGTTCATCTCCTGACGTG	816

QY	342	-----AlaLysGlyThrSerCysAsnGlnArg	350
DB	817	GACTGGAGCTACGGTGAGCCAAACCGAGATGTTATGCCGGTCCCAATGATGAGAGGGG	876
QY	351	LeuGluArgIleSerGlyThrGlnHisThrIleLeuArgValProPheArgAsnGlu	370
DB	877	ATGGGTGAGAGTGGCGA-----GCTACATTGTGGCATACCGTCT-----	918
QY	371	AsnGlyIleLeuLysLysTrpIleSerArgPheAspValTrpProTyrLeuGluThrPhe	390
DB	919	---GGCCCGCGGATAAATACCTCAAGAAAGAGCGTTGTGGCTTACCTCCCAAGAGCTT	975
QY	391	AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly	404
DB	976	GTCGATGGAGCCCTTGGCGATATCTGAACATGTCAGGCTCTGGAGAGCAGGTGGA	1035
QY	405	Thr-----ProAspPheIleIleGlyAsnTyrSerAspGlyAsnLeuVal	419
DB	1036	AATGGAGGCGCAGTACTGCTTACGTGATACATGGGCACCTATCGCATGCTGGAGATGT	1095
QY	420	AlaSerLeuLeuSerTyrIysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu	439
DB	1096	GCTGCTCTCTTCTGCTGGCTGAATGTGCCAATGCTCTGCTGCCACTCCTCTGGG	1155
QY	440	LysThrLys-----TyrProAspSerAspIlePheTrpLysAsnPheAspGlu	455
DB	1156	AGGAACAAGCTGGACAACCTGCTGAAGCAGGCGGATGTCGAAGGAGAGATCGATCG	1215
QY	456	LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAlaAspPhe	475
DB	1216	ACATACAGATCATGAGGCGTATCGAGGCTGAGGAGCTGGCCCTGGATGCTCAGAGCTT	1275
QY	476	IleIleThrSerTyrGlnGluIleAlaGlySerIysAsnThrValGlyGlnTyrGlu	495
DB	1276	GTAATCAGCAGCACAGGCGAGAGATTGAT-----GAGCAGTGG---	1314
QY	496	SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal---	514
DB	1315	-----GGATTGTAC-----GATGATTGATTGATCAAG	1341
QY	515	-----PheAsp	516
DB	1342	CTTGACAAAAGTCTGAGGCGACCGGCGAGCGCGGGTGTAGCTGCCATGCTCGTTACATG	1401
QY	517	ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu	536
DB	1402	CCTGAGATGGTGGTATTCTCCGGGAATGGATTTCGCAATGTTGTAGTTCTAT-----	1455
QY	537	LysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGlu	556
DB	1456	-----GAACACATTGATGGGATGGTAC	1479
QY	557	GlnAsnAspGluHisIleGly-----	563
DB	1480	GTCAAAAGATGATATCGTTGTGTTTGGAGGGTGCCTCACCAAGTCAATGCCCAATTGG	1539
QY	564	-----HisLeuAspAspArgSerIysProIleLeuPheSerMetAlaArg	578
DB	1540	GCGAAGTATGCGGTTCTCTGACCACTTCACAGCCGATGATCTCGGCGTTATCAAGA	1599
QY	579	LeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeu	598
DB	1600	CCAGACCCGAGAGAGACATCACTACCTCGTCAAGCCCTTTGGAGAGTGTCTGCCACTC	1659
QY	599	ArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSerLysAsp	618
DB	1660	AGGGAACCTTGCAACCTTACTCTCTGATCATGGGTACAGAGATGATCGACGATGTCT	1719
QY	619	ArgGluGluIleAlaGluLeuGluLysMetHisGluLeuIleLysThrHisAsnLeuPhe	638
DB	1720	GCTGGCAATGCCAGTGTCTCTCACCAAGTCTTGAGCTGATTGACAGTATGATCTGATC	1779
QY	639	GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg	658

1780	DB	GGAGCGTGGCTTC---CCTAAGCATCAACAATCAGGCTCAGCTCCGGAGATCTATCGC	1836
659	QY	TyrI ¹ caAlaAspThrHisgIlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu	678
1837	DB	CTCGCGCCAAATGAGGGCGTCTTCATCAACCTGCTCTCGTTGACCGTTTGGTCTC	1896
679	QY	ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyLeuGlyPro	698
1897	DB	ACCTGATCGAGGCTGGGCACACGGACTCCCGATAGTCGCTACCAAGAATGTTGGTCCG	1956
699	QY	AlaGluIleLeuGluHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln	718
1957	DB	GTCGACATTACAATGCAATTAACACAGGACTGCTGTTCAACCCACACAGCACCAG----	2010
719	QY	AlaValAsnLeuMetAlaAspPhePheAspArgCysIysGlnAspProAspHisTyrVal	738
2011	DB	-----AAGCCCATCGCTGAAGCACTGCTGAAGCTTGTGCACACAGAACCCTGTGGCAG	2064
739	QY	AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluIysTyrThrTrpIysIleTyrSer	758
2065	DB	GAAATCGCGGAGAAACGGGCTTGGCAATCCAC---CTCTACTATGCGCGGAGCACTGC	2121
759	QY	GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTyrIysTyrValSerLysLeu	777
2122	DB	CGNCATTCCTACCACGCGGTGGCGGTGC-----	2151
778	QY	GluArgLeuGluThrArgArgTyrLeuGlu	787
2152	DB	---CGGTAAAGGAACCGGAGCTGGCTGAAG	2178

RESULT, T 7

US-09-078-862-2	Sequence 2, Application US/09078862	Db	757	ATGATGCTGGAGGTACAGGGTGACCTTCTACTGTGCAAGTGTCTATCTCCAGCTG	816
Patent No. 6091003	GENERAL INFORMATION:	Qy	342	-----AlaLysGlyThrSerCysAsnGlnArg	350
APPLICANT: Nan, Guo-Ling	APPLICANT: Nagai, Chifumi	Db	817	GACTGGAGCTACGGTGAGCCAAACGAGATGTTATGCGCGGTTCCAATGAGGAGGGG	876
APPLICANT: Medlen & Carroll, LLP	STREET: 220 Montgomery Street, Suite 2200	Qy	351	LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu	370
CITY: San Francisco	STATE: California	Db	877	ATGGGTGAGAGTGGCGGA-----GCCTACATTGTGCGCATACCGTGT	918
COUNTRY: United States of America	ZIP: 94104	Qy	371	AsnGlyIleLeuLysLysTrpIleSerArgPheAspValTrpProTyrLeuGluThrPhe	390
COMPUTER READABLE FORM:	MEDIUM TYPE: Floppy disk	Db	919	---GGGCGCGGATTAATACCTCAGAGGAAGCGTTGTGGCTTACTCTCCAGAGTTT	975
COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MS-DOS	Qy	391	AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly	404
SOFTWARE: PatentIn Release #1.0, Version #1.30	CURRENT APPLICATION DATA:	Db	976	GTGATGGAGCCCTTGGCGCATATCTGAACATGTCCAAGGCTCTGGGAGAGCAGGTTGGA	1035
FILING DATE: 14-MAY-1998	CLASSIFICATION: 800	Qy	405	Thr-----ProAspPheIleIleGlyAsnTyrSerAspGlyAsnLeuVal	419
ATTORNEY/AGENT INFORMATION:	NAME: Carroll, Peter G.	Db	1036	AATGGAGGCCAGTACTGCCTTACGTGATACATGGGCGACTATGCGGATGCTGGAGAGTT	1095
REGISTRATION NUMBER: 32,837	REFERENCE/DOCKET NUMBER: UH-03321	Qy	420	AlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu	439
TELECOMMUNICATION INFORMATION:	TELEPHONE: (415) 705-8410	Db	1096	GCTGCTCTCTTCTGTGGCGCTGAAATGTGCCAATGGTCTCCTACCTGCCCATCTACCTGG	1155
TELEFAX: (415) 397-8338	INFORMATION FOR SEQ ID NO: 2:	Qy	440	LysThrLys-----TyrProAspSerAspIlePheTrpLysAsnPheAspGlu	455
SEQUENCE CHARACTERISTICS:	LENGTH: 3509 base pairs	Db	1156	AGGAACAAGCTGGAAACAACCTGCTGAAGCAAGGGCGCATGTCCAAGGAGGAGATCGATTCG	1215
TYPE: nucleic acid	STRANDEDNESS: single	Qy	456	LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPhe	475
TOPOLOGY: linear	MOLECULE TYPE: cDNA	Db	1216	ACATACAAGATCATGAGGCGTATCGAGGGTGAGAGCTGGCGCTGGATGCGTCAGAGCTT	1275
		Qy	476	IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu	495
		Db	1276	GTATCAGACACACAGCGAGAGATTGAT-----GACCATGG-----	1314
		Qy	496	SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal	514
US-09-078-862-2		Db	1315	-----GATGGATTGATGTCAG	1341

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QY 515 -----PheAsp 516
Db 1342 CTTGAGAAAGTGTGAGGCGACGGGAGCGGGGTAGTCCCATGTCGTACATG 1401
QY 517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
Db 1402 CCTAGATGGTGTGATCTCTCGGATGATTTAGCAATGTTAGTTCAT-----1455
QY 537 LysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGlu 556
Db 1456 -----GAGACATGATGGGATGGTGC 1479
QY 557 GlnAsnAspGluHisIleGly-----563
Db 1480 GTCAAGATGATATCGTTGTTGGAGGTGCTCCACCAAGTCAATGCCCCCAATTGG 1539
QY 564 -----HisLeuAspAspArgSerLysProIleLeuPheSerMetAlaArg 578
Db 1540 GCGGAAGTATGCGGTTCCTGACCAACCTCACAGCCGATGATCTCGGCGTTATCAAGA 1599
QY 579 LeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeu 598
Db 1600 CCAGACCCGAGGAAGAACATCACTACCTCGTCAAGCGTTTGAGAGTCTCGTCCACTC 1659
QY 599 ArgGluLeuValAsnLeuValValAlaGlyTyrAsnAspValAsnLysSerLysAsp 618
Db 1660 AGGAATCTGCAACCTTACTGTATGTTGGTAAACAGATGATGATGATGATGATGATG 1719
QY 619 ArgGluLeuIleAlaGluIleGluLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
Db 1720 GCTGGCAATGCCAGTGTCTCCACACAGTCTGAAGCTGATGACAAAGTATGATCTGATC 1779
QY 639 GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
Db 1780 GGAAGCGTGGCGTTC-----CCTAAGCATCAACAATCAGCTCCCGAGATCTATCCG 1836
QY 659 TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
Db 1837 CTCGGCCCAAAATGAAGGGCGTCTTCAACCTGCTCTGTTGAGCGTTGGTCTC 1896
QY 679 ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
Db 1897 ACCCTGATCGAGCTGGGCGACACGAGTCCCGATAGTCCGATACCAAGAATGGTGGTCCG 1956
QY 699 AlaGluIleLeuGluHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
Db 1957 GTCGACATTAACAATGATTAACAACGAGTCTGCTGTTGACCCACACAGCCAG-----2010
QY 719 AlaValAsnLeuMetAlaAspPhePheAspArgCysLysGlnAspProAspHisTrpVal 738
Db 2011 -----ACGCCATCGTGTGACTGCTGAAGCTTGTGGCAGACAGAACCTGTGGCAG 2064
QY 739 AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTrpLysIleTyrSer 758
Db 2065 GAATGCGGAGAAACGGGCTCGGCAATCCAC---CTCTACTCATGGCCGAGCACTGC 2121
QY 759 GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTrpLysTyrValSerLysLeu 777
Db 2122 CGCACTTACCTCACAGGGTGGCGGGTGC-----2151
QY 778 GluArgLeuGluThrArgArgTyrLeuGlu 787
Db 2152 ---CGGTTAGGAACCCGAGTGGCTGAAG 2178
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RESULT 8

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; US-051-341-6
; Sequence 6, Application US/09251341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shemwaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
```

```
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter, Ph.D.,
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.110.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4400
TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURES:
NAME/KEY: CDS
LOCATION: 112..3315
US-09-051-341-6
Alignment Scores:
Pred. No.: 1,84e-40 Length: 3509
Score: 444.00 Matches: 159
Percent Similarity: 40.48% Conservative: 96
Best Local Similarity: 25.24% Mismatches: 211
Query Match: 10.45% Indels: 164
DB: 3 Gaps: 24
US-10-080-114a-12 (1-809) x US-09-051-341-6 (1-3509)
QY 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleGlnAla 260
Db 532 GGAGACACCATCGCGAGCTT-----GCG 555
QY 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle-----276
Db 556 CCGGTTGAGACGACCAAGAGAGTTCACAGGAGAACTTCTCTGACCTTACCGTCTGGTCT 615
QY 277 -----PheAsnValValValSerProHisGlyTyrPhe---288
Db 616 GACGACATTAAGAGAGAGAGCTTACATTGCTGCTCATCGGTCGATGCTGTTGCT 675
QY 289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
Db 676 GGAGAAAACATCGGAACCTAGTCTCGGTGATTCGATACAGTGGCCAGGTGAAATATGTCGTC 735
QY 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysGlnGlyLeuAsp 327
Db 736 GAACTTCAAGAGCG-----ATGTCA 756
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QY	328	ValSerPro-----LysileLeuileValThrArgLeulle-----ProAsp----	341
Db	757	ATGATCGCTGGAGTGACAGGGTGGACCTCTTCACTCGTCAAGTGTCACTCTCGTCAAGTG	816
QY	342	-----AlaLysGlyThrSerCysAsnGlnArg	350
Db	817	GACTGGAGCTACGGTGAGCCAAACCGAGATGTTATGCGCGGTTCCAAATGATGATGAGAGGGG	876
QY	351	LeuGluArgileSerGlyThrGlnHisThrTyrlleLeuArgValProPheArgAsnGlu	370
Db	877	ATGGGTGAGAGTGGCGGA-----GCTACATTTGGGCATACCGTGT-----	918
QY	371	AsnGlyileLeuLysTyrIleSerArgPheAspValTrpProTyrIleuGluThrPhe	390
Db	919	---GGGCCCGGGATTAACACTCTCAAGAAGAGACCGTTGTGGCTTACCTCTCCAAGAGTTT	975
QY	391	AlaGluAspAlaAlaGlyGluile-----AlaAlaGluLeuGlnGly	404
Db	976	GTGATGGGAACCTTGGCGGATATCTGTAACATGTTCCAGGCTCTGGAGAGACAGTGTGA	1035
QY	405	Thr-----ProAspPheIlelleGlyAsnTyrSerAspGlyAsnLeuVal	419
Db	1036	AAATGGAGGCCACTACTGCTTACGTGATACATGGCCACTATGCCGATGCTGGAGATGT	1095
QY	420	AlaSerLeuLeuSerTyrIysMetGlylleThrGlnCysAsnIleAlaHisAlaLeuGlu	439
Db	1096	GTGCTCTCTCTTCTGTGCTGCTGAATGTCCTCAATGGTGTCTCATCGCCACTCACTTGGG	1155
QY	440	LysThrLys-----TyrProAspSerAspIlePheTrpIysAsnPheAspGlu	455
Db	1156	AGGAACAAGCTGGAAACAATGCTGAACGACGAGCGGCATGTCACGAGGAGGATCGATTG	1215
QY	456	LysTyrHisPheSerCysGlnPheThrAlaAspIlelleAlaMetAsnAsnAlaAspPhe	475
Db	1216	ACATACAAGATCATGAGCGTATCGAGGGTGAGGAGCTGCGCCGTGATGCGTCAGAGCTT	1275
QY	476	IlelleThrSerThrTyrlngInGluilleAlaGlySerIysAsnThrValGlyGlnTyrGlu	495
Db	1276	GTAAATCAAGACGACAAAGCGCAGGAGATGTAT-----GAGCAGTGTG-----	1314
QY	496	SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal---	514
Db	1315	-----GGATGTAC-----GATGATTTGATGTCAAG	1341
QY	515	-----PheAsp	516
Db	1342	CTTGAGAAAGTGTGAGGCAACGGCGAGGCGGGGTAGCTGCCATGTGCTTACATG	1401
QY	517	ProLysPheAsnIleValSerProGlyAlaAspMetSerileTyrPheProHisThrGlu	536
Db	1402	CCATGATGTGTGTATCTCTCGGGATGGATTTTACGAAATCTGTAGTTCAT-----	1455
QY	537	LysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGlu	556
Db	1456	-----GAGACATTCATGGGATGCTGAC	1479
QY	557	GlnAsnAspGluHisIleGly-----	563
Db	1480	GTCAAAGATCATATGCTGTGTTTGGAGGTGCTCATCCCAAGTCAATGCCCCCAATTGG	1539
QY	564	-----HisLeuAspAspArgSerIysProIleLeuPheSerMetAlaArg	578
Db	1540	GCCGAGTGTATGCGTTCCTGACCAACCTCAACAGCGATGATCTCTGGGGTATCAAGA	1599
QY	579	LeuAspArgValLysAsnIleThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeu	598
Db	1600	CCAGACCGAAGAAACATCACTACCTCGTCAAAGCCTTGGAGAGTGTCTGCCATC	1659
QY	599	ArgGluLeuValAsnLeuValValAlaGlyTyrAsrAspValIasnIysSerIysAsp	618
Db	1660	AGGGAACCTTGCAACCTTACTCTGATCATCGGTAAACAGAGATGACATCGACGACATGTCT	1719

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Qy 619 ArgGluGluLeuAlaGluIleGlyLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
Db 1720 GCTGGCAATGCCAGTGTCTCACACAGCTTCTGAAGCTGATTGCACAGTAGTATGCTGTAC 1779
Qy 639 GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
Db 1780 GGAAGCGTGGCTTC---CCTAAGCATCAAAATCAGGCTCGCTCCGGAGATCTATCGC 1836
Qy 659 TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
Db 1837 CTCGGCCCAAAATGAAGCGCTTCATCAACCCCTCTCTCGTTGAGCGTTGGTCTC 1896
Qy 679 ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
Db 1897 ACCCTGATCGAGCTGGCGCACACGGACTCCCGACTCCCGATGTCGTACTACCAAGAATGGTGGTCCG 1956
Qy 699 AlaGluIleLeuHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
Db 1957 GTGACATTACAATGCAATTAAACACGGACTGCTGTTGACCCACACGACCGAG----- 2016
Qy 719 AlaValAsnLeuMetAlaAspPhePheAspArgCysLysGlnAspProAspHisTrpVal 738
Db 2011 -----NACGCCATCGCTGATGCACTGCTGAAGCTTGGCAGACAGAAGCTGTGGCAG 2064
Qy 739 AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGlnLysTyrThrTrpLysIleTyrSer 758
Db 2065 GAATGCCGGAGAAACGGGCTGGCGCAACATCCAC---CTCTACTCATGGCCGGAGCACTGC 2121
Qy 759 GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTrpLysTyrValSerLysLeu 777
Db 2122 CGCACTTACTCTACAGGGTGGCGGGTGC----- 2151
Qy 778 GluArgLeuGluThrArgArgTyrLeuGlu 787
Db 2152 ---CGGTTAAGAACCCGAGGTGGCTGAAG 2178

RESULT 9
US-09-866-153-12
; Sequence 12, Application US/09866153
; Patent No. 6638766
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; ATTORNEY: Wei, Hailong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; PRIORITY FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Zea mays
US-09-866-153-12

Alignment Scores:
Pred. No.: 1,84e-40 Length: 3509
Score: 444.00 Matches: 159
Percent Similarity: 40.48% Conservative: 96
Best Local Similarity: 25.24% Mismatches: 211
Query Match: 10.45% Indels: 164
DB: 4 Gaps: 24

US-10-080-114A-12 (1-809) x US-09-866-153-12 (1-3509)

Qy 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuAspIleIleGlnAla 260
Db 532 GGAGACCACTCGCGAGCTT-----GCG 555
Qy 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276

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Db 556 CCGTTTGAGACGACCAAGAAGATTCCAGAGAACTTCTCTGACCTTACCGTCTGGTCT 615
Qy 277 -----PheAsnValValSerProHisGlyTyrPhe--- 288
Db 616 GACGACAAATAGGAGAGAGAGCTTACATTTGCTCTCATCAGCTGCATGCTTGTTCGT 675
Qy 289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
Db 676 GAGAGAAACATGCAACTAGTCTGTGATTCGTATACAGTGCAGGAGTGAAATATGTGTC 735
Qy 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysLysGlnGlyLeuAsp 327
Db 736 GAATTCGCAAGACG-----ATGTC 756
Qy 328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
Db 757 ATGATCGCTGGAGTGTACAGGCTGACCTCTTCTACCTGCTCAAGTGTCTCTCTGAGTG 816
Qy 342 -----AlaLysGlyThrSerCysAsnGlnArg 350
Db 817 GACTGGAGCTACGGTGAGCCACCGAGATGTTATGCGCCGGTTCCMATGATGAGAGGGG 876
Qy 351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
Db 877 ATGGGTGAGAGTGGCGA-----GCCATATTGTGGCATACCGTGT----- 918
Qy 371 AsnGlyIleLeuLysLysTrpIleSerArgPheAspValTrpProTyrLeuGluThrPhe 390
Db 919 ---GGCCCGGGGATAAATACCTCMAGAGGAGCGTTGTGGCTTACTTCCAGAGTTT 975
Qy 391 AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
Db 976 GTGATGGAAGACCTTGGCGATATCTCTGAACATGTCCAAAGGCTCTGGGAGAGCGATTGGA 1035
Qy 405 Thr-----ProAspPheIleIleGlyAsnTrpSerAspGlyAsnLeuVal 419
Db 1036 AATGGAGGCCAGTACTGCTTACGTGATATACATGGGCACATGCGGATGCTGGAGATGTT 1095
Qy 420 AlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu 439
Db 1096 GCTGCTCTCTTCTTCTGGTGGCTGAATGTCCCAATGCTGCTCACTGCCACTCACTTGGG 1155
Qy 440 LysThrLys-----TyrProAspSerAspIlePheTrpLysAsnPheAspGlu 455
Db 1156 AGGAACAAGCTGAACAACACTGCTGAAGCAAGGCGCATGTCCAAGGAGAGATCGATTTCG 1215
Qy 456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPhe 475
Db 1216 ACATACAAGATCATGAGGCGTATCGAGGCTGAGGAGCTGCGCCCTGGAGCGTTCAGAGCTT 1275
Qy 476 IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu 495
Db 1276 GTATATCAGGACACAGGACGAGAGATTGAT-----GAGCAGTGG--- 1314
Qy 496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal--- 514
Db 1315 -----GATGATTTGATGTCAAG 1341
Qy 515 -----PheAsp 516
Db 1342 CTTGAGAACTGCTAGGCGCAGCGCGGGGTTAGTCCCATGCTCGTATCATG 1401
Qy 517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
Db 1402 CCTAGGATGTTGGTATCTCTCCGGGAATGATTTTCAGCAATGTTGTAGTTCAT----- 1455
Qy 537 LysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGlu 556
Db 1456 -----CAAGACATTGATGGGATGGTGAC 1479
Qy 557 GluAsnAspGluHisIleGly----- 563
Db 1480 GTCAAGATGATATCGTTGGTTTGGAGGTCCTCCACCCCAAGTCAATGCCCCCAATTGG 1539

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Qy 564 -----HisLeuAspArgSerLysProIleLeuPheSerMetAlaArg 578
Db 1540 GCGGAAGTGATGGTTCCTTGACCAACCTCACAAGCCGATGATCTCTGGCGTTATCAAGA 1599
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Db 1600 CCGAACCCGAGAGAACATCACTACCTCGTCAAGCGTTTGGAGAGTGTCTGCCACTC 1659
Qy 599 ArgGluLeuValAsnLeuValAlaGlyTyrAsnAspValAsnLysSerLysAsp 618
Db 1660 AGGAACCTTCAACCTTACTCTGATCTGGTGAACAGATGACATCGACGATGCTCT 1719
Qy 619 ArgGluGluIleAlaGluIleGlyLysMetHisGluLeuIleLysThrHisAsnLeuPhe 638
Db 1720 GCTGGCAATCCAGTGTCTCCACACAGCTTCTGAAGCTGATTGACAAAGTATGATCTGAC 1779
Qy 639 GlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArg 658
Db 1780 GGAAGCGTGGCGTTC---CCTAAGCATCAACAATCAGCTGACGTCCTCCGGAGATCTATCGC 1836
Qy 659 TyrIleAlaAspThrHisGlyAlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeu 678
Db 1837 CTGCGGCCAAATGAAGCGGTCTTCTCAACCTGCTCTCTGTTGAGCCGTTTGGTCTC 1896
Qy 679 ThrValValGluAlaMetThrCysGlyLeuProThrPheAlaThrLeuHisGlyGlyPro 698
Db 1897 ACCTGATCGAGCTGCGGCACACGGACTCCGATAGCTACCAAGAATGTTGGTCCG 1956
Qy 699 AlaGluIleLeuGluHisGlyValSerGlyPheHisIleAspProTyrHisProGluGln 718
Db 1957 GTGACATTTCAAAATGCAATTAACACACGACTGCTGTTGCCACACACGACCGAG--- 2010
Qy 719 AlaValAsnLeuMetAlaAspPheAspArgCysLysGlnAspProAspHisTrpVal 738
Db 2011 -----AACCCATCGCTGATGACTGCTGAAGTGTGGCAGACAGAACCTGTGGCAG 2064
Qy 739 AsnIleSerGlyAlaGlyLeuGlnArgIleTyrGluLysTyrThrTrpLysIleTyrSer 758
Db 2065 GAATGCGGAGAAACGGCTGCGCAACATCCAC---CTCTACTCATGCGCGAGCACTGC 2121
Qy 759 GluArgLeuMetThr---LeuAlaGlyValTyrGlyPheTrpLysTyrValSerLysLeu 777
Db 2122 CGCACTTACCTACCCAGGCTGCGCGGTGC--- 2152
Qy 778 GluArgLeuGluThrArgArgTyrLeuGlu 787
Db 2152 ---CGTTAAGGACCCGAGGTGCTGAAG 2178

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RESULT 10

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US-09-693-467A-12
; Sequence 12, Application US/09693467A
; Patent No. 6686513
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: UH-04331
; CURRENT APPLICATION NUMBER: US/09/693,467A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3509
; TYPE: DNA
; ORGANISM: Zea mays
US-09-693-467A-12

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Alignment Scores: 1.84e-40 Length: 3509
Pred. No.: 444.00 Matches: 159
Score:

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Percent Similarity: 40.48% Conservative: 96
 Best Local Similarity: 25.24% Mismatches: 211
 Query Match: 10.45% Indels: 164
 DB: 4 Gaps: 24

US-10-080-114A-12 (1-809) x US-09-693-467A-12 (1-3509)

QY 241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGluAla 260
 |||||
 Db 532 GGAGACACCATCGCGAGCTT-----GCG 555

QY 261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276
 |||||
 Db 556 CCGGTGAGACGACCAAGAGAGAGTTCAGGAGAACTTCTGACCTACCGTCTGGTCT 615

QY 277 -----PheAsnValValValSerProHisGlyTyrPhe----- 288
 |||||
 Db 616 GACGACAAATAGGAGAGAAAGCTTTACATTGTGCTCATCAGCGTGCATGTGTTGCT 675

QY 289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
 |||||
 Db 676 GGAGAAACATGGAATGAGTGTGATCTGATACAGGTGGCCAGGTCGAATATGTGCTC 735

QY 308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysLysGlnGlyLeuAsp 327
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 Db 736 GAACCTGCAGAGCG-----ATGCA 756

QY 328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
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 Db 757 ATGATGCTGGAGTGTACAGGTGGAGCTCTTCACTCGTCAAGTGTCAATCTCTGAGCTG 816

QY 342 -----AlaLysGlyThrSerCysAsnGlnArg 350
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 Db 817 GACTGGAGCTACGCTGAGCCACCGAGATGTATGCGCCGGTTCATGATGAGAGAGGGG 876

QY 351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
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 Db 877 ATGGGTGAGAGTGGCGA-----GCCTACATTGCGCATACCGTGT----- 918

QY 371 AsnGlyIleLeuLysTyrIleSerArgPheAspValTyrProTyrLeuGluThrPhe 390
 |||||
 Db 919 ---GGGCGCGGATAAATACCTCAAGAGAAAGCGTTGTGGCTTACCTCCAGAGATT 975

QY 391 AlaGluAspAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
 |||||
 Db 976 GTCGATGGAGCCCTTGGCATATCTGAACATGTCCAGGCTCTGGAGAGACGATTGGA 1035

QY 405 Thr-----ProAspPheIleIleGlyAsnTyrSerAspGlyAsnLeuVal 419
 |||||
 Db 1036 AATGGGAGGCGAGTACTGCTTACGTGATACATGGGCACATATGCGGATGCGGAGATGTT 1095

QY 420 AlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu 439
 |||||
 Db 1096 GCTGCTCTCTCTTCTGGTGGCTGAATGTCACCAATGGTGTCTACCTGGCCCATCTCACTTGG 1155

QY 440 LysThrLys-----TyrProAspSerAspIlePheTyrLysAsnPheAspGlu 455
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 Db 1156 AGGAACAGCTGGAACACATGCTGAAGCAAGCGGCATGTCCAGAGGAGATCGATTG 1215

QY 456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAlaAspPhe 475
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 Db 1216 ACATACAGATCATGAGCGGTATGAGGAGGAGGCTGCGCTGGATGCGTCAGAGCTT 1275

QY 476 IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu 495
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 Db 1276 GTAATCAGAGACCAAGGAGGAGATGAT-----GAGCAGTGG--- 1314

QY 496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal--- 514
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 Db 1315 -----GGATTGTAC-----GATGGATTGTGATGTCAG 1341

QY 515 -----PheAsp 516
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RESULT 11

US-08-356-354-3

; Sequence 3, Application US/08356354

; Patent No. 5767365

; GENERAL INFORMATION:

; APPLICANT: SONNEWALD, Uwe

; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

; TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen

STREET: 1180 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/C8/356,354
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US PCT/EP93/01605
FILING DATE: 22-JUN-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: DE P42 20 758.4
FILING DATE: 24-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Yeilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
FEATURE:
NAME/KEY: CDS
LOCATION: 121..3282
OTHER INFORMATION: /note= "Sucrose-Phosphate-Synthase"
08-356-354-3

137	PheGluProCpheAsnValSerValProArgProAsnA	gSerSer	leGlyAsnGly	156
70	TTCTACTCCGTTAACTCTCTAGCACACGGCGGAGGAGTGGCGGAGGAGATGCGGGA	129		
157	ValGlnPheLeuAsnA	rgHisSerSerleMetPheArgAsnA	ArgAspCysleuGlu	176
130	AACGNATTGGATTAAACAGTTAC		-----TTAGAG	156
177	ProLeuLeuAspPheLeuArgGlyHisA	rgHis	slyGlyHisValMetMetLeuAsnA	196
157	GGCATACTGGATGTTTGGACACAGGGCTAGATGATAAGAACTCATCGTTGTTGTGTAGAGAA	216		
197	ArgIleGlnSerLeuGlyA	rg	-----LeuGlnSerValleuThr	209
217	AGA-----GGGAGGTTT	AGTCTCGACGAGTACTTGTGTTGAGAA	TTTATTACT	264
210	LysAlaGluGlu-----HisLeuSerLysLeuProAla		-----	220
265	CGATTTCGATTGACACTGATTGTCATCGTTCG--GGATCCGAGACAAGTACTCTCGAGTCCG	324		

Db	385	AAAAGCAGCTTGAGGGAGAGCAAGCTCAGTGGATGCAAAACACCCGCTCAAGAACGTA	444
Qy	248	GLuMet----	250
Db	445	AGAGTGGCAGAGAAAGCAGTTCGTGATATGTCAGAGGATCTATCTGAGGAGAGAAAGGA	504
Qy	251	-----TleHisLeuLeuLeuAspIleleleAlaProAspProSerTh	265
Db	505	GATATAGTCGCTGACATGTCATCTCATG-----GTGAAGTACCAGAGCGCGATG	555
Qy	265	rLeuGluLysPheLeu-----GlyArgIleProMetIl	276
Db	556	CCTAGAATCAGTTCGTGTGACAAATGGAAGCATGGGTCACTCAGCAGAGAGAAAGAG	615
Qy	276	ePheAsnValValValSerProHisGlyTyrPhe---GlyGlnAlaAsnValLeuGl	295
Db	616	CTTTAT-ATCGTGTATAGATTACATGGTTTAATTCGGGGTGAGAAATATGAGAGCTTGG	674
Qy	295	YLeu---ProAspThrGlyGlyGlnIleValTyrIleLeuAspGlnValArgAlaLeuGl	314
Db	675	ACGGGATTCGATACTGGTGTGAGTGAAGTATGTTGTTGAACTTCGAGGSCCTTAGG	734
Qy	314	uAsp-----GluMetValLeuArgLeuLysLysGlnGlyLeuAs	327
Db	735	GTCCATGCCAGGTGTATATCGGTGTGACTTGTCTACTAGACAATCT-----	783
Qy	327	pValSerProLysIle-----LeuIleValThrArgLeuIl	339
Db	784	---TCACCAAGATGATGGAGCTATGGTACCCAGCAGAGATGCTGACGCCATTAAG	839
Qy	339	eProAspAlaLysGlyThrSerCysAsnGlnArgLeuGluArgIleSerGlyThrGlnHi	359
Db	840	TACAGCGGCTTGATGACTGAGATGGGGAG-----AGTAGTGG	878
Qy	359	sThrTyrIleLeuArgValProPheArgAsnGluAsnGlyIleLeuLysLysTrpIleSe	379
Db	879	TGCTTATATTATCCGATTCCTTT-----GGACCAAGAGAGAAATATATTC	926
Qy	379	rArgPheAspValTrpProTyrLeuGluThrPheAlaGluAspAla-----	394
Db	927	AAAAGACAGCTATGGCCCTATATCCGAAATTTGTGATGGTGCACTTAACCATATAT	986
Qy	395	---AlaGlyIleAlaAlaGluLeuGlnGlyThr-----ProAspPh	408
Db	987	TCAATGTCCAAAGTCTTGGGAGCAAAATGGTAGTGGCTATCTGTGTGGCTGTTC	1046
Qy	408	eIleIleGlyAsnTyrSerAspGlyAsnLeuValAlaSerLeuLeuSerTyrLysMetGl	428
Db	1047	CATACCGGACATATGCTGATGCTGCGCATCTCAGCTGCTCTCTCTCAGGTGCTTAAA	1106
Qy	428	YIleThrGlnCysAsnIleAlaHisAlaLeuGluLysThrLysTyr-----	443
Db	1107	TGTACCAATGCTTTTCACTGCTCACTCCTGTTAGTGAAGTGGAGCACTGTGGC	1166
Qy	444	-----ProAspSerAspIlePheTrpLysAsnPheAspGluLysTyrHisPheSe	460
Db	1167	ACAAGTGGAAAGTCAAAGAT-----GAAATAAATCAACCTCAGATAAT	1214
Qy	460	rCysGlnPheThrAlaAspIleIleAlaMetAsnAlaAspPheIleIleThrSerTh	480
Db	1215	CGCGAGATAGAGGCTGAAGAATTAACCTCTTGATGCTTCCGAATTTGTCATCACTAGTAC	1274
Qy	480	rTyGlnGlnIleAlaGlySerLysAsnThrValGlyGlnTyrGluSerHisThrAlaPh	500
Db	1275	AAGCAGAGAGATTGAC-----GAGCAATGGCGCTTGTATGATGGGTT	1316
Qy	500	eThrLeuProGlyLeuTyrArgValValHisGly-----Il	512
Db	1317	TGAT---CCATATTAGAGCTAAGTACGTGGCAGGATCAGCGCAATGTCAGCTGTTA	1373
Qy	512	eAspValPheAspProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPh	532

1374 TGGCAGGTTTATGCCCTCGTATGGCTGTAAATTCCTCTCGGATGGAGTTCCACCATATGT 1433

Qy 532 eProHisThrGluLysAlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuI 552

Db 1434 GCACATGAGAGTGCACATGATGGTGAACA-----GAGGAAGTGAAGTGGGAAGAC 1487

Qy 552 eTyAspProGluGlnAsnAspGluHisIleGlyHisLeuAspAspArgSerIysProI 572

Db 1488 CCGGATCCACCTATTGGGCAGAGATTATGGCTTCTTTTCTAAATCCAAGGAAGCCTAT 1547

Qy 572 eLeuPheSerMetAlaArgLeuAspArgValIysAsnIleThrGlyLeuValGluAlaPh 592

Db 1548 GATATCGCATCTGCTAGGCTGATCCCAAGAGAACCCTCACTACTTTAGTGAAGCAATT 1607

Qy 592 eAlaLysCysAlaLysLeuArgGluLeuValAsnLeuValValAlaGlyTyraAsnAs 612

Db 1608 TGGTGAATGTCGCATTGAGAGAGCTTGCTAATCTTACTTGAATATGGTGAATCGAGA 1667

Qy 612 pValAsnLysSerIysAspArgGluGluIleAlaGluIleGluLysMethHisGluLeuI 632

Db 1668 TATATCGACGAATGCTAGCACCAATCTGCACCTCTCTCTTCAATCTTGAATATGAT 1727

Qy 632 eLysThrHisAsnLeuPheGlyGlnPheArgTrpIleSerAlaGlnThrAsnArgAlaAr 652

Db 1728 AGATAAGTATGATCTTTATGGTCAAGTAGCTTAT--CCTAAACACCAAGCAGTCCAGA 1784

Qy 652 gAsnGlyGluLeuTyArgTrpIleAlaAspThrHisGlyAlaPheValGlnProAlaLe 672

Db 1785 TGTTCTGTATATCTACCGCTCTTGCTGCAAGACATGAGGGTGTTTATTATATCCAGCTTT 1844

Qy 672 uTyrGluAlaPheGlyLeuThrValValGluAlaMetThrCysGlyLeuProThrPheAl 692

Db 1845 TATTGAGCCTTTTGAGCTGACTTTGATTGAGGCAGCAGCTTATGGTCTCCCAATGGTAGC 1904

Qy 692 aThrLeuHisGlyClyProAlaGluIleIleGluHisGlyVal-----SerGlyPheHi 710

Db 1905 CACAAAATATGGAGACCTGTGTATATA-----CATAGGGTCTTCACCAATGGTCTCTTT 1958

Qy 710 sIleAspProTyHisProGluGlnAlaValAsnLeuMetAlaAspPhePheAspArgCy 730

Db 1959 AGTGGATCCC---CTGATCAGCAGGCAATTT-----GCTGATGCTCTTTGAAGTT 2006

Qy 730 sLysGlnAspProAspHisTrpValAsnIleSerGlyAlaGlyLeuGlnArgIleYrGl 750

Db 2007 GATTGCTGATAAGCAACTGTGGCTGAATGCAGGCAATGGATTAAAAAATATCCAC-- 2064

Qy 750 uLysTyThrTrp-----LysIleTySerGluArgLeu 761

Db 2065 -CTTTTCTATGCGCCGAGCAGCTGTAAACTTATCTATCCCGGATA 2109

RESULT 13

US-08-553-436A-5

? Sequence 5, Application US/08553436A

? Patent No. 5866790

? GENERAL INFORMATION:

? APPLICANT: HESSE, Holger

? APPLICANT: MULLER-ROBER, Bernd

? TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

? TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE

? TITLE OF INVENTION: CONCENTRATION

? NUMBER OF SEQUENCES: 8

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: Oetrolenk, Faber, Gerb & Soffen

? STREET: 1180 Avenue of the Americas

? CITY: New York

? STATE: NY

? COUNTRY: US

? ZIP: 10036-8403

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible

? OPERATING SYSTEM: PC-DOS/MS-DOS

? SOFTWARE: PatentIn Release #1.1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,436A
 FILING DATE: 17-NOV-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP94/01671
 FILING DATE: 20-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 4317596.1
 FILING DATE: 24-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weillman, Edward
 REGISTRATION NUMBER: 24,735
 REFERENCE/DOCKET NUMBER: P/951-117
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 382-0700
 TELEFAX: (212) 382-0888
 TELEX: 236925
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3635 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Beta vulgaris
 INDIVIDUAL ISOLATE: Saccharosephosphate Synthase
 IMMEDIATE SOURCE:
 LIBRARY: phage lamda zap
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 30..3167
 US-08-553-436A-5

Alignment Scores:
 Pred. No.: 3,81e-40 Length: 3635
 Score: 441.50 Matches: 146
 Percent Similarity: 45.50% Conservative: 102
 Best Local Similarity: 26.79% Mismatches: 190
 Query Match: 10.40% Indels: 107
 DB: 2 Gaps: 24

US-10-080-114A-12 (1-809) x US-08-553-436A-5 (1-3635)

QY 279 ValValValValSerProHisGlyTyrPhe---GlyGlnAlaAscValLeuGlyLeu--- 296
 DB 516 CTGTGTTTGAATAGTCTTCATGGTTTGTATGAGGTGAAACATGGAACCTTGGCCGTGAT 575
 QY 297 ProAspThrGlyGlyGlnIleValTyrIleLeuAspGlnValArgAlaLeuGluAsnGlu 316
 DB 576 TCTGATACTGGTGGTCAGGTTAAGTATGTGCTGAGCTTGCAGGGCTCTAGGTTTCGATG 635
 QY 317 -----MetValLeuArgLeuLysLysGlnGlyLeuAspVal 328
 DB 636 CCAGGTGTTTATAGTGTATTTGCTAAGTACAGGCAAGTTTCATCTCCTGAGCTGGATGG 695
 QY 329 Ser-----ProLysIleLeuValThrArgLeuIleProAspAlaLysGlyThr 345
 DB 696 AGTTATGGGAGGCTACTGAGTCTGAATCCAAAG-----GATCCAAATGGTTT 746
 QY 346 SerCysAsnGlnArgLeuGluArgIleSerGlyThrGlnHisThrIleLeuArgVal 365
 DB 747 GATGATGATGAT-----GATGAATGGGAGAGTAGTGTGCTTACATGTTTCGTATA 800
 QY 366 PropheArgAsnGluAsnGlyIleLeuLysLysTrpIleSerArgPheAspValTrpPro 385
 DB 801 CCATTT-----GGGCCGAGGATGATATATCGCAAAAGAGAGCTTGGCCC 848
 QY 386 TyrLeuGluThrPheAlaGluAspAlaAlaGlyGluIleAla----- 399
 DB 849 TATATTCCTGAATTTGTTGAGTGGCTCTAAACCCACATAGTTCAAATGTCCAAAGTTTAA 908

QY 400 AlaGluLeuGlnGlyThr-----ProAspPheIleIleGlyAsnTyrSer 414
 DB 909 GGTGAGCAAAATGGTAGCGGGGAAACAGTTTGGCCAGTTGCCATTCATGCACATATGCT 968
 QY 415 AspGlyAsnLeuValAlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIle 434
 DB 969 GATGCTGGTGTATCTGCTGCTCTTCTTCTGGTGGCTTAAATGTTCCATGCTTTTAAACG 1028
 QY 435 AlaHisAlaLeuGluLysThrLysTyrProAsp----- 445
 DB 1029 GGGCATTTCTTGGCCGACAGCAAGTTAGACAGCTCTCTCAACAGGGTCAATGTCTAA 1088
 QY 446 SerAspIlePheTrpLysAsnPheAspGluLysTyrHisPheSerCysGlnPheThrAla 465
 DB 1089 GATGACATA-----AACATACATACAAATAATAGCTAGGATAGAGCC 1133
 QY 466 AspIleIleAlaMetAsnAsnAlaAspPheIleIleThrSerThrTyrGlnGluIleAla 485
 DB 1134 GAAGAGTTTATCATTGATGCTCTGAGATAGTCATACTAGTACAAACAAGAAATAGAA 1193
 QY 486 GlySerLysAsnThrValGlyGlnTyrGluSerHisThrAlaPheThrLeuProGlyLeu 505
 DB 1194 -----GAGCAATGGCCACTCTATGATGGGTTTGAAT---CCTGTGCTA 1232
 QY 506 -----TyrArgValValHisGlyIleAspVal-----PheAspPro 517
 DB 1233 GAACGTAAACTCCGTGCTAGGATGAGCGTGGTGAAGCTGTTATGGAGGTTTCATGCC 1292
 QY 518 LysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGluLys 537
 DB 1293 CGGATGGTTGTTATTTCTCTCTGGAATGGAATTCATCATATATTTCCACAT----- 1343
 QY 538 AlaLysArgLeuThrSerLeuHisGlySerIleGluAsnLeuIleTyrAspProGluGln 557
 DB 1344 -----GAGGGTGTATATGATGATGATGAT-----GAAACAGAGAA 1373
 QY 558 AsnAspGluHis-----IleGlyHisLeu 565
 DB 1374 ACTGAAGAGCATCTTACATCATCCACTATCTCGGGGTGAGATTATGGCTCTT 1433
 QY 566 AspAspArgSerLysProIleLeuPheSerMetAlaArgLeuAspArgValLysAsnIle 585
 DB 1434 TCTAAACCAAGAACCAATGATCTTGCCTTGTAGGCTGACCCGAGAGAAATATC 1493
 QY 586 ThrGlyLeuValGluAlaPheAlaLysCysAlaLysLeuArgGluLeuValAsnLeuVal 605
 DB 1494 ACGACTTGGTCAAGCATTTGGAGATGCCGCTCCACTAAGGAGAGCTAGCTAATCTTACT 1553
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 DB 1614 CTGTCACTGGTTAGCTAAATGATCAATACGACCTTTATGGTCAAGTAGCATAC---CCC 1670
 QY 646 AlaGlnThrAsnArgAlaArgAsnGlyGluLeuTyrArgTyrIleAlaAspThrHisGly 665
 DB 1671 AAACATCAACAGCAAGCATGATGTTCTCGAGATTATGCTTTGGCAGCAACAGCAAGGGA 1730
 QY 666 AlaPheValGlnProAlaLeuTyrGluAlaPheGlyLeuThrValValGluAlaMetThr 685
 DB 1731 GTCTTTTATTAATCCAGCTTTTATGAGCCATTTGGGCTGACTCTTAATAGAGGACAGCT 1790
 QY 686 CysGlyLeuProThrPheAlaThrLeuHisGlyGlyProAlaGluIleIleGluHisGly 705
 DB 1791 CATGTTTACCGATGGTGTCTCGCAAAATGGAGCCCTGTTGATATCCAGAGGCTCCT 1850
 QY 706 ValSerGlyPheHisIleAspProTyrHisProGluGlnAlaVal----- 720
 DB 1851 GATAATGGTCTTCTGTGGGATCTCT---CATGAGCAGAGCTATTGTCTACTGCTTTGCTG 1907
 QY 721 AsnLeuMetAlaAsp-----PhePheAspArgCysLysGlnAspProAspHisTrpVal 738

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Db      1908 AAGCTTGTTCTCATAGCAAACTATGACAAAAATGCCAGCAAAAT----- 1952
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Qy      739 AsnIleSerGlyAlaGlyLeuGlnAArgIleTyrGluLysTyrThrTropLysIleTyrSer 758
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1953 -----GACCTGAAATAATATTCAT---CTCTACTCTTGCCAGAGCATTCG 1994
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      759 GluArgLeuMetThr 763
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1995 AAGACATACCTATCT 2009
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RESULT 14
US-08-429-054A-12
: Sequence 12, Application US/38429054A
: Patent No. 5917126
: GENERAL INFORMATION:
: APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
: APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
: TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
: TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
: TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIERMAN AND MUSERLIAN
: STREET: 600 THIRD AVENUE
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: USA
: ZIP: 10016
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/429,054A
: FILING DATE: 26-APR-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 842,337
: FILING DATE: 20-March-1992
: APPLICATION NUMBER: PCT/FR 91/00593
: FILING DATE: 18-July-1991
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: French 96402094.9
: FILING DATE: 20-July-1990
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Charles A. Musierlian
: REGISTRATION NUMBER: 19,683
: REFERENCE/DOCKET NUMBER: 146.1137
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 661-8000
: TELEFAX: (212) 661-8002
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3509
: TYPE: Nucleic acid
: STRANDEDNESS: Unknown
: TOPOLOGY: Unknown
: MOLECULE TYPE: CDNA
US-08-429-054A-12

Alignment Scores:
Pred. No.: 1.55e-39 Length: 3509
Score: 436.00 Matches: 161
Percent Similarity: 40.79% Conservative: 96
Best Local Similarity: 25.56% Mismatches: 209
Query Match: 10.27% Indels: 164
DB: 2 Gaps: 26

US-10-080-114a-12 (1-809) x US-08-429-054A-12 (1-3509)

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Qy      241 GlyAspThrAlaGlyHisValLeuGluMetIleHisLeuLeuLeuAspIleIleGlnAla 260
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Db      532 GGAACACCATCGAGAGAGCTT-----GCG 555
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Qy      261 ProAspProSerThrLeuGluLysPheLeuGlyArgIleProMetIle----- 276
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      556 CCGGTTGAGACGACCAAGAAGAGTTCACAGAGAACTTCTCTGACCTTACCGTCTGGTCT 615
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Qy      277 -----PheAsnValValValSerProHisGlyTyrPhe----- 288
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      616 GACGACAAATAAGGAGAGAAAGCTTTACATTGTGTCATCAGCGTCGTCGTTGTTGCT 675
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      289 GlyGlnAlaAsnValLeuGlyLeu---ProAspThrGlyGlyGlnIleValTyrIleLeu 307
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      676 GGAAGAAACATGGAACCTAGTCTGTGATCTGTATACAGGTGCCAGGTGAATATGTGGTC 735
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      308 AspGlnValArgAlaLeuGluAsnGluMetValLeuArgLeuLysGlnGlyLeuAsp 327
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      736 GAACCTGCAAGAGCG-----ATGTC 756
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      328 ValSerPro-----LysIleLeuIleValThrArgLeuIle-----ProAsp--- 341
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      757 ATGATGCTCGAGGTGTACAGGGTGGACCTCTTCACTCGTCAAGTGTCACTCTCTGACGTG 816
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      342 -----AlaLysGlyThrSerCysAsnGlnArg 350
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      817 GACTGGAGTACGGTGAGCCAAACCGAGATGTTATGCCCGGTTCCATGATGGAGAGGGG 876
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      351 LeuGluArgIleSerGlyThrGlnHisThrTyrIleLeuArgValProPheArgAsnGlu 370
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      877 ATGGGTGAGAGTGGCGGA-----GCCTACATTGTGGCATACCGTGT----- 918
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      371 AsnGlyIleLeuLysTyrIleSerArgPheAspValTyrProTyrLeuGluThrPhe 390
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      919 ---GGGCCGCGGATTAATACCTCAAGAGAGACGGTGTGGCGCTTACCTCCAAGAGTT 975
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      391 AlaGluAspAlaAlaGlyGluIle-----AlaAlaGluLeuGlnGly 404
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      976 GTCGATGGAGCCCTTGGCATATCTCTGAACATGTCACAGGCTCTGGGAGAGAGAGTTGGA 1035
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      405 -----ThrProAspPheIleIleGlyAsnTyrSerAspGlyAsnLeuVal 419
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1036 ATTGGGAGGCCAGTACTACTCTTACGTGATACATGCGGCACCTATGCGGATCTGGAGATGT 1095
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      420 AlaSerLeuLeuSerTyrLysMetGlyIleThrGlnCysAsnIleAlaHisAlaLeuGlu 439
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1096 GCTGCTCTCTTCTTGTGCTGCGTGAATGCTCCAAATGCTCTCACTGGCCACTCACTTGGG 1155
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      440 LysThrIys-----TyrProAspSerAspIlePheTyrLysAsnPheAspGlu 455
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1156 AGGACAAAGCTGGAAACAACCTGCTGAAGCAAGGCGCATGTCCAAGAGAGAGATCGATTCG 1215
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      456 LysTyrHisPheSerCysGlnPheThrAlaAspIleIleAlaMetAsnAsnAlaAspPhe 475
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1216 ACATACAGATCATGAGCGGTATCGAGGGGTGAGAGAGCTGCGCCCTGGATGGTCAAGACTT 1275
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      476 IleIleThrSerThrTyrGlnGluIleAlaGlySerLysAsnThrValGlyGlnTyrGlu 495
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1276 GTATCAGGACCAAGCGCAGAGATGAT-----GAGCAGTGG--- 1314
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      496 SerHisThrAlaPheThrLeuProGlyLeuTyrArgValValHisGlyIleAspVal--- 514
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1315 -----GGATTGTAC-----GATGATTGTATGTCAG 1341
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      515 -----PheAsp 516
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1342 CTTGAGAAAGTCTGAGGGCAGCGGCGAGCGCGGGGTAGCTGCCATGCTCGTTACATG 1401
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Qy      517 ProLysPheAsnIleValSerProGlyAlaAspMetSerIleTyrPheProHisThrGlu 536
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::
Db      1402 CTTAGGATGGTGTGATCTCTCCGGAAATGGATTTCAGCAATGTTGTAGTTTCAT----- 1455
      |||:::|||||::: |||:::|||||::: |||:::|||||::: |||:::|||||:::

```


